

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2002, 15:49:31 ; Search time 13 seconds  
(without alignments)  
56.367 Million cell updates/sec

Title: US-09-720-828A-4  
Perfect score: 147  
Sequence: 1 APTSSSTKKTQLEHLLDLOMILNGINN 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues  
Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued.Patents.AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCITUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfilest.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	100.0	31	4	US-09-116-594-2
2	147	100.0	50	1	US-08-127-351-13
3	147	100.0	50	1	US-08-480-367B-13
4	147	100.0	50	1	US-08-487-221A-13
5	147	100.0	50	1	US-08-480-370-13
6	147	100.0	88	4	US-08-817-787-15
7	147	100.0	96	1	US-08-160-376A-5
8	147	100.0	96	1	US-08-389-487-8
9	147	100.0	133	1	US-07-800-366-1
10	147	100.0	133	1	US-08-354-456A-5
11	147	100.0	133	1	US-08-225-224-3
12	147	100.0	133	1	US-08-318-193-89
13	147	100.0	133	1	US-08-284-393B-1
14	147	100.0	133	1	US-08-284-393B-2
15	147	100.0	133	1	US-08-284-393B-3
16	147	100.0	133	1	US-08-734-471-1
17	147	100.0	133	3	US-08-722-258-3
18	147	100.0	133	4	US-08-817-787-13
19	147	100.0	133	4	US-09-310-026-1
20	147	100.0	133	5	PCR-US95-04468-3
21	147	100.0	133	5	PCR-US95-08950-1
22	147	100.0	133	5	PCR-US95-08950-2
23	147	100.0	133	5	PCR-US95-08950-3
24	147	100.0	133	6	5210029-1
25	147	100.0	133	6	5256769-1
26	147	100.0	133	6	5464939-2
27	147	100.0	134	6	5496924-55

28	147	100.0	153	3	US-09-012-366-3	Sequence 3, Appl
29	147	100.0	153	4	US-08-759-628-8	Sequence 8, Appl
30	147	100.0	153	4	US-09-522-217-111	Sequence 11, App
31	147	100.0	153	6	5314995-7	Patent No. 5314995
32	147	100.0	157	4	US-08-818-562-2	Sequence 2, Appl
33	147	100.0	157	4	US-08-155-888-2	Sequence 2, Appl
34	147	100.0	504	4	US-07-932-915-2	Sequence 2, Appl
35	147	100.0	504	5	PCR-US91-05826-2	Sequence 2, Appl
36	144	98.0	251	3	US-08-875-811-59	Sequence 59, Appl
37	144	98.0	254	3	US-08-875-811-61	Sequence 61, Appl
38	143	97.3	133	1	US-08-354-456A-6	Sequence 6, Appl
39	132.5	90.1	127	3	US-08-806-121B-3	Sequence 3, Appl
40	102	69.4	141	4	US-08-930-917A-18	Sequence 18, Appl
41	79	53.7	135	2	US-08-383-621-5	Sequence 5, Appl
42	79	53.7	135	3	US-08-459-906-5	Sequence 5, Appl
43	79	53.7	1098	1	US-07-777-715-7	Sequence 7, Appl
44	79	53.7	1098	1	US-08-170-126-2	Sequence 2, Appl
45	79	53.7	1098	3	US-08-954-418-2	Sequence 2, Appl

## ALIGNMENTS

```

RESULT 1
US-09-116-594-2
; Sequence 2, Application US/09116594
; Patent No. 6168785
; GENERAL INFORMATION:
; APPLICANT: THEZE, Jacques
; APPLICANT: ECKENBERG, Ralph
; APPLICANT: MOREAU, Jean-Claude
; APPLICANT: MAZIE, Jean-Claude
; TITLE OF INVENTION: BIOLOGICAL APPLICATIONS OF NEW PEPTIDES OF IL-2 AND
; TITLE OF INVENTION: DERIVATIVES AND USE AS THERAPEUTIC AGENTS
; FILE REFERENCE: 0660-0134-0
; CURRENT APPLICATION NUMBER: US/09/116,594
; CURRENT FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-116-594-2

Query Match      100.0%; Score 147; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APTSSSTKKTQLEHLLDLOMILNGINN 30
   |||||||
DB 2 APTSSSTKKTQLEHLLDLOMILNGINN 31

RESULT 2
US-08-127-351-13
; Sequence 13, Application US/08127351
; Patent No. 5449761
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, WAITER &
; ADDRESSEE: NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400

```

TELEX:  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/127,351  
FILING DATE: 28-SEP-1993  
CLASSIFICATION: 534  
ATTORNEY/AGENT INFORMATION:  
NAME: Villacorta, Gilberto M.  
REGISTRATION NUMBER: 34,038  
REFERENCE/DOCKET NUMBER: 4980-004-44  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR-SEO ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-127-351-13

Query Match 100.0%; Score 147; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 3.4e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLLEHLLDLMILNGINN 30  
DB 1 APTSSSTKKTQQLLEHLLDLMILNGINN 30

RESULT 3  
US-08-480-367B-13  
Sequence 13, Application US/08480367B  
Patent No. 5578288  
GENERAL INFORMATION:  
APPLICANT: BELINKA Jr, BENJAMIN A.  
APPLICANT: COUGHLIN, DANIEL J.  
APPLICANT: ALVAREZ, VERNON L.  
APPLICANT: WOOD, RICHARD  
TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE  
TITLE OF INVENTION: CONSTRUCTS  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER  
STREET: 99 Canal Center Plaza, Suite 300  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,367B  
FILING DATE: 07-06-95  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Villacorta, Gilberto M.  
REGISTRATION NUMBER: 34,038  
REFERENCE/DOCKET NUMBER: 2654-002A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 684-1111  
TELEFAX: (703) 684-1124

TELEX:  
INFORMATION FOR SEO ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-480-367B-13

Query Match 100.0%; Score 147; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 3.4e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLLEHLLDLMILNGINN 30  
DB 1 APTSSSTKKTQQLLEHLLDLMILNGINN 30

RESULT 4  
US-08-487-221A-13  
Sequence 13, Application US/08487221A  
Patent No. 5593656  
GENERAL INFORMATION:  
APPLICANT: BELINKA Jr, BENJAMIN A.  
APPLICANT: COUGHLIN, DANIEL J.  
APPLICANT: ALVAREZ, VERNON L.  
APPLICANT: WOOD, RICHARD  
TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE  
TITLE OF INVENTION: CONSTRUCTS  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,221A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/127,351  
FILING DATE: 28-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Villacorta, Gilberto M.  
REGISTRATION NUMBER: 34,038  
REFERENCE/DOCKET NUMBER: 4980-004-44  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR-SEO ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-487-221A-13

Query Match 100.0%; Score 147; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 3.4e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLLEHLLDLMILNGINN 30  
DB 1 APTSSSTKKTQQLLEHLLDLMILNGINN 30

```
RESULT 5
US-08-480-370-13
; Sequence 13, Application US/08480370
; Patent No. 5609847
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,370
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-480-370-13

Query Match      100.0%; Score 147; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 APTSSSTKKTQLEHLHLLDLMILNGINN 30
DB      1 APTSSSTKKTQLEHLHLLDLMILNGINN 30

RESULT 6
US-08-817-787-15
; Sequence 15, Application US/08817787
; Patent No. 6294353
; GENERAL INFORMATION:
; APPLICANT: Pack, Peter
; APPLICANT: Lupas, Andrei
; TITLE OF INVENTION: TARGETED HETERO-ASSOCIATION OF
; TITLE OF INVENTION: RECOMBINANT PROTEINS TO MULTI-FUNCTIONAL COMPLEXES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
```

```
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,787
; FILING DATE: 23-SEP-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04117
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94 11 6558.1
; FILING DATE: 20-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 88 amino acids
; TYPE: amino/acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-817-787-15

Query Match      100.0%; Score 147; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 6.8e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 APTSSSTKKTQLEHLHLLDLMILNGINN 30
DB      3 APTSSSTKKTQLEHLHLLDLMILNGINN 32

RESULT 7
US-08-160-376A-5
; Sequence 5, Application US/08160376A
; Patent No. 5473049
; GENERAL INFORMATION:
; APPLICANT: Obermeier, Ranier
; APPLICANT: Gerl, Martin
; APPLICANT: Ludwig, Jurgen
; APPLICANT: Sabel, Walter
; TITLE OF INVENTION: Process For Obtaining Prolinsulin
; TITLE OF INVENTION: Possessing Correctly Linked
; TITLE OF INVENTION: Cystine Bridges
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth A. Genoni, Esq.
; STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500
; CITY: Somerville
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08876-1258
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 386
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/160,376A
; FILING DATE: December 1, 1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: GE P 4240420.7  
FILING DATE: December 2, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Barbara V. Maurer, Esq.  
REGISTRATION NUMBER: 31,287  
REFERENCE/DOCKET NUMBER: HOE 92/F 384  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 231-4079  
TELEFAX: (908) 231-2255  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 Amino Acids  
TYPE: Amino Acid (AA)  
TOPOLOGY: not relevant  
US-08-160-376A-5

Query Match 100.0%; Score 147; DB 1; Length 96;  
Best Local Similarity 100.0%; Pred. No. 7.6e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLDLMILNGINN 30  
DB 2 APTSSSTKKTQLEHLLDLMILNGINN 31

RESULT 8  
US-08-389-487-8  
Sequence 8, Application US/08389487  
Patent No. 5663291  
GENERAL INFORMATION:  
APPLICANT: Obermeier, Rainier  
APPLICANT: Gerl, Martin  
APPLICANT: Ludwig, Jurgen  
APPLICANT: Sabel, Walter  
TITLE OF INVENTION: Process for Obtaining Insulin Having  
TITLE OF INVENTION: Correctly Linked Cysteine Bridges  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/389,487  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Einaudi, Carol P.  
REGISTRATION NUMBER: 32,220  
REFERENCE/DOCKET NUMBER: 02481.1424-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-389-487-8

Query Match 100.0%; Score 147; DB 1; Length 96;  
Best Local Similarity 100.0%; Pred. No. 7.6e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLDLMILNGINN 30  
DB 2 APTSSSTKKTQLEHLLDLMILNGINN 31

RESULT 9  
US-07-800-366-1  
Sequence 1, Application US/07800366  
Patent No. 5250296  
GENERAL INFORMATION:  
APPLICANT: OOTSU, Koichihiro  
TITLE OF INVENTION: IMMUNOSTIMULANT AGENT CONTAINING  
TITLE OF INVENTION: INTERLEUKIN-2 AND 5'-DEOXY-5-FLUOROURIDINE  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &  
ADDRESS: CUSHMAN  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/800,366  
FILING DATE: 19911127  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Castle, Donald R.  
REGISTRATION NUMBER: 24,220  
REFERENCE/DOCKET NUMBER: 41417(281)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-800-366-1

Query Match 100.0%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLDLMILNGINN 30  
DB 1 APTSSSTKKTQLEHLLDLMILNGINN 30

RESULT 10  
US-08-354-456A-5  
Sequence 5, Application US/08354456A  
Patent No. 5567611  
GENERAL INFORMATION:  
APPLICANT: Ralph, Peter  
APPLICANT: Martin, George  
APPLICANT: Platek, Michael  
APPLICANT: Larrick, James W.  
TITLE OF INVENTION: Multifunctional M-CSF Proteins and Genes Encoding  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: Intellectual Property - R440, P.O. Box 8097  
CITY: Emeryville

STATE: California  
COUNTRY: U.S.A.  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/354,456A  
FILING DATE: 12-DEC-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/995,338  
FILING DATE: 21-DEC-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McCarfigle Jr., Philip L.  
REGISTRATION NUMBER: 31,395  
REFERENCE/DOCKET NUMBER: 750,003/32387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2718  
TELEFAX: (510) 653-3542  
TELEX: n/a  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-354-456A-5

Query Match 100.0%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1,1e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTSSSTKTKTQLOLEHLLDLQMLNGINN 30  
Db 1 APTSSSTKTKTQLOLEHLLDLQMLNGINN 30

RESULT 11  
US-08-225-224-3  
Sequence 3, Application US/08225224  
Patent No. 5635599  
GENERAL INFORMATION:  
APPLICANT: PASTAN, Ira  
APPLICANT: KREITMAN, Robert J.  
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND  
TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: Stewart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,224  
FILING DATE: 8-APR-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 15280-193  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..133  
OTHER INFORMATION:  
US-08-225-224-3 /label= IL2

Query Match 100.0%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1,1e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTSSSTKTKTQLOLEHLLDLQMLNGINN 30  
Db 1 APTSSSTKTKTQLOLEHLLDLQMLNGINN 30

RESULT 12  
US-08-318-193-89  
Sequence 89, Application US/08318193  
Patent No. 5641663  
GENERAL INFORMATION:  
APPLICANT: GARVIN, Robert T.  
APPLICANT: MAHER, Lawrence T.  
TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION  
TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY  
TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/318,193  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,314  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 18740/116 CACO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-9300  
TELEFAX: (703) 883-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-318-193-89

Query Match 100.0%; Score 147; DB 1; Length 133;

Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APTSSSTKKTQLOLEHLLDQIMLINGINN 30  
Db 1 APTSSSTKKTQLOLEHLLDQIMLINGINN 30

## RESULT 13

US-08-284-393B-1

Sequence 1, Application US/08284393B

Patent No. 5696234

GENERAL INFORMATION:

APPLICANT: Zurawski, Sandra M.

APPLICANT: Zurawski, Gerard

TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/284,393B

FILING DATE: 01-AUG-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0389

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-852-9196

TELEFAX: 415-496-1200

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 133 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-284-393B-1

Query Match 100.0%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1.1e-15;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APTSSSTKKTQLOLEHLLDQIMLINGINN 30  
Db 1 APTSSSTKKTQLOLEHLLDQIMLINGINN 30

## RESULT 14

US-08-284-393B-2

Sequence 2, Application US/08284393B

Patent No. 5696234

GENERAL INFORMATION:

APPLICANT: Zurawski, Sandra M.

APPLICANT: Zurawski, Gerard

TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/284,393B

FILING DATE: 01-AUG-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0389

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-852-9196

TELEFAX: 415-496-1200

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 133 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-284-393B-2

Query Match 100.0%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APTSSSTKKTQLOLEHLLDQIMLINGINN 30  
Db 1 APTSSSTKKTQLOLEHLLDQIMLINGINN 30

## RESULT 15

US-08-284-393B-3

Sequence 3, Application US/08284393B

Patent No. 5696234

GENERAL INFORMATION:

APPLICANT: Zurawski, Sandra M.

APPLICANT: Zurawski, Gerard

TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/284,393B

FILING DATE: 01-AUG-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0389

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-852-9196

TELEFAX: 415-496-1200

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 133 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

• Mon Oct 28 09:43:45 2002

MOLECULE TYPE: peptide  
US-08-284-393B-3

Query	March	Similarity	100.0%	Score	147	DB 1	Length	133
Best Local	Similarity	100.0%	Pred.	No. 1	1e-15			
Matches	30	Conservative	0	Mismatches	0	Indels	0	Gaps
Oy	1	APTSSSTKKTQLOLEHLLLDLQMLINGINN	30					
Db	1	APTSSSTKKTQLOLEHLLLDLQMLINGINN	30					

Search completed: October 25, 2002, 15:53:05  
Job time : 13 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2002, 15:43:41 ; Search time 31 Seconds

(without alignments)  
111.074 Million cell updates/sec

Title: US-09-720-828A-2

Perfect score: 152

Sequence: 1 MAPSSSTKKTQLQLLEHLIDQLMGLNGINN 31

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
A\_Geneseq\_032802:\*  
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	152	100.0	31	21	AAV51597
2	152	100.0	38	12	AA11015
3	152	100.0	60	11	AA10638
4	152	100.0	60	15	AA18245
5	152	100.0	96	15	AA18899
6	152	100.0	96	16	AA18662
7	152	100.0	133	13	AA12595
8	152	100.0	134	5	AA14050
9	152	100.0	134	6	AA15053
10	152	100.0	134	6	AA15085
11	152	100.0	134	7	AA16102

12	152	100.0	134	8	AA170585
13	152	100.0	134	11	AA105267
14	152	100.0	134	11	AA105266
15	152	100.0	134	11	AA105240
16	152	100.0	136	20	AA149917
17	152	100.0	143	15	AA10932
18	152	100.0	149	11	AA107265
19	152	100.0	149	11	AA107266
20	152	100.0	149	11	AA107267
21	152	100.0	149	11	AA107269
22	152	100.0	149	11	AA107148
23	152	100.0	149	11	AA107149
24	152	100.0	149	11	AA107150
25	152	100.0	149	11	AA107261
26	152	100.0	149	11	AA107262
27	152	100.0	149	11	AA107263
28	152	100.0	149	11	AA107264
29	152	100.0	172	10	AA194809
30	152	100.0	201	11	AA106839
31	152	100.0	255	6	AA150305
32	152	100.0	273	6	AA150087
33	152	100.0	273	6	AA150310
34	152	98.0	65	10	AA191032
35	149	98.0	149	11	AA107146
36	149	98.0	149	11	AA107268
37	149	98.0	149	11	AA107255
38	149	98.0	149	11	AA107256
39	149	98.0	149	11	AA107257
40	149	98.0	149	11	AA107258
41	149	98.0	149	11	AA107259
42	149	98.0	381	22	AA112707
43	149	98.0	421	17	AA195055
44	149	98.0	435	12	AA111273
45	149	98.0	496	17	AA195058

# ALIGNMENTS

RESULT 1	AAV51597	standard; Protein; 31 AA.
ID	AAV51597	
AC	AAV51597	
DF	25-MAY-2000	(first entry)
XX		
DE	Human IL-2 derived peptide IP130 #1.	
XX		
KW	IL-2; interleukin 2; human; IP130; immunosuppressive; antirheumatic; graft rejection; autoimmune disorder; rheumatoid arthritis.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200004048-A1.	
XX		
PD	27-JAN-2000.	
XX		
PF	16-JUL-1999;	99MO-IB01424.
XX		
PR	16-JUL-1998;	98US-0116594.
XX		
PA	(INSP ) INST PASTEUR.	
XX		
PI	These J, Eckenberg R, Moreau J, Goldberg M, Rose T, Alzari P; Mazie J;	
XX		
DR	WPI; 2000-182403/16.	
XX		
PT	N-PSDB; AA288837.	
XX		
PT	Novel cytokine peptides and antibody for preventing and/or treating undesirable immune reactions e.g. graft rejection and autoimmune disorders	
PT		

Sequence of human  
Sequence of natura  
Sequence of natura  
Sequence of natura  
Human interleukin  
tbl. Synthetic.  
Recombinant Interl  
Recombinant Interl  
Recombinant Interl  
Recombinant Interl  
Recombinant Interl  
Recombinant Interl  
Recombinant Interl  
Human interleukin  
Human IL-2 N-termi  
Fused antibody rec  
Conjugate of inter  
Interferon-gamma a  
Human interleukin-  
Recombinant Interl  
Recombinant Interl  
Recombinant Interl  
Recombinant Interl  
Recombinant Interl  
Recombinant Interl  
Human bIVPH1-IL-2  
IL-2-DETA-DGALA mu  
HSV-1 antigen/heat  
GALA-DT-IL-2 mult

```

XX PS Claim 1; Page 54; 56pp; English.
CC CC This invention describes a novel a peptide, IP130 having 31 (I) or 30
CC (II) amino acid sequence or its homologous sequence (H) exhibiting the
CC same activity or binding characteristic. The products of the invention
CC have immunosuppressive and antirheumatic activity. (I) or (II) is used
CC for preparing medicament useful to induce IL-2 activity (A) or a peptide
CC binding to it is used for inhibiting the activity of IL-2R in treating
CC conditions related with undesirable immune reactions like graft
CC rejection, and autoimmune disorders like rheumatoid arthritis. It is also
CC used for immunofluorescence purification of native or recombinant IL-2
CC peptides. (V) is also used for preparing medicaments in treating patients
CC with deficient IL-2 activity. (III) used to prepare antisense
CC oligonucleotides and ribozymes modulating the expression of IL-2 which
CC can be used in gene therapy applications. The peptides inhibits or mimics
CC the binding of helix A of IL-2 to a subunit of an IL-2R and thus produces
CC a specific interaction. This sequence represents an IP130 peptide
CC described in the method of the invention.
CC XX
SQ Sequence 31 AA;
Query Match 100.0%; Score 152; DB 21; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.3e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPTSSSTKKTQQLQLEHLLDLMILGINN 31
DB 1 MAPTSSSTKKTQQLQLEHLLDLMILGINN 31
RESULT 2
AAR1015
XX ID AAR1015 standard; Peptide; 58 AA.
XX AC AAR1015;
XX DT 13-MAY-1991 (first entry)
XX DE Human Interleukin-2-derived stabiliser peptide.
XX KW Interleukin-2; IL-2; gag 24; gp 41; gp 36; HIV detection.
XX OS Homo sapiens.
XX PN EP416673-A.
XX PD 13-MAR-1991.
XX PF 02-AUG-1990; 90EP-0202108.
XX PR 03-AUG-1989; 89CU-0000149.
XX RA (INCE-) CENT ING GENETICA.
XX PI Novoa Perez LJ, Machado Lahera JA, Fernandez Maso JR;
XX PI Bentez Fuentes JV, Nardicandi Diaz RE, Rodriguez Reinoso JL;
XX PI Estrada Garcia MP, Garcia Suarez J, Herrera Martinez LS;
XX WI: 1991-075192/11.
XX DR N-PSDB; AAO10898.
XX PT Method for expressing heterologous proteins - as fusion protein,
XX PT using vector contg. stabilising sequence
XX PS Claim 2; Page 10; 18pp; English.
CC CC The sequence corresponds to the first 58 amino acid residues of
CC human IL-2. It forms part of a fusion protein, linked to a
CC heterologous protein. The heterologous protein is preferably gag 24
CC or a fragment of gp 41 of HIV-1 or it is a fragment of gp 36 of
CC HIV-2. Such fusion proteins can be used to detect antibodies to
CC these proteins. See also AAO10899-Q10903.

```

```

XX SQ Sequence 58 AA;
Query Match 100.0%; Score 152; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 4.6e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPTSSSTKKTQQLQLEHLLDLMILGINN 31
DB 1 MAPTSSSTKKTQQLQLEHLLDLMILGINN 31
RESULT 3
AAR06838
XX ID AAR06838 standard; protein; 60 AA.
XX AC AAR06838;
XX DT 14-JAN-1991 (first entry)
XX DE Human IL-2 N-terminal transcript of plasmid pT13S.
XX KW Bovine tuberculosis; Interleukin-2; IL-2; plasmid pT13S.
XX OS Mycobacterium bovis.
XX PN JP02195895-A.
XX PD 02-AUG-1990.
XX PF 24-JAN-1989; 89JP-0013270.
XX PR 24-JAN-1989; 89JP-0013270.
XX PA (AJIN ) AJINOMOTO KK.
XX DR WPI; 1990-278851/37.
XX DR N-PSDB; AAO05976.
XX PT BCG bacteria derived immuno:protein MPB70 - can be used as
XX PT diagnostic agent used to determine bovine tuberculosis.
XX PS Disclosure; Fig 2; 11pp; Japanese.
XX CC Immunoprotein MPB 70 encoding sequence may be incorporated into
XX CC plasmid pT13S with an N-terminal fragment of human IL-2. The plasmid
XX CC may be used to transform an expression system giving a fusion
XX CC protein which may be used as a diagnostic agent for bovine
XX CC tuberculosis infection.
XX SQ Sequence 60 AA;
Query Match 100.0%; Score 152; DB 11; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.8e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPTSSSTKKTQQLQLEHLLDLMILGINN 31
DB 1 MAPTSSSTKKTQQLQLEHLLDLMILGINN 31
RESULT 4
AAR48245
XX ID AAR48245 standard; Protein; 60 AA.
XX AC AAR48245;
XX DT 12-JUL-1994 (first entry)
XX DE Human Interleukin-2.
XX KW non-coding region; coding region; resonance; interaction; IL-2;
KW optimisation; degenerate sequence; plasmid pT13Sneo; PT9-11;

```

KM gene expression; regulation; recombinant protein production;  
 KM Interleukin-2; Interleukin-6.  
 OS Homo sapiens.  
 PN FR2692594-A.  
 XX 24-DEC-1993.  
 PD  
 XX 22-JUN-1992; 92PR-0007571.  
 PF  
 XX 22-JUN-1992; 92PR-0007571.  
 PR  
 XX (PERE/) PEREZ J.  
 PA  
 PI Perez J;  
 XX  
 DR WPI: 1994-028256/04.  
 XX N-PSDB; AA055629, AA055630.  
 PT Application of optimised gene expression - for scientific,  
 PT Industrial and therapeutic purposes  
 PS Disclosure: Fig 28 and Fig 29; 110pp; French.  
 CC Resonances between coding and non-coding regions were measured for  
 CC the native human IL-2 gene in plasmid p911 (see AA055630) and a  
 CC synthetic IL-2 gene (AA055629) in which alternative, degenerate  
 CC codons were used in order to introduce additional restriction  
 CC sites. It was found that the degenerate changes greatly upset the  
 CC "natural order" between coding and non-coding regions: as a result,  
 CC the amount of protein expressed by the degenerate gene is likely to  
 CC be adversely affected. The inventors have proposed an "optimised"  
 CC IL-2 gene with the aim of increasing the amount of protein expressed  
 CC by the gene. (N.B. the sequence is also described as  
 CC Interleukin-6).  
 CC  
 SQ Sequence 60 AA;  
 Query Match 100.0%; Score 152; DB 15; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 4, 8e-14;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MAPSSSTKKTQLOLEHLDDLQMLINGINN 31  
 DB 1 MAPSSSTKKTQLOLEHLDDLQMLINGINN 31  
 RESULT 5  
 AAR68899 standard; peptide; 96 AA.  
 AC AAR68899;  
 XX  
 DT 02-MAR-1995 (first entry)  
 XX  
 DE Human pro-insulin 2.  
 XX  
 KM Pro-insulin; A-chain; B-chain; C-chain; disulphide;  
 KM mercaptan; chaotropic agent.  
 OS Homo sapiens.  
 XX  
 OS EP600372-A.  
 PN  
 XX  
 PD 08-JUN-1994.  
 PF  
 XX 25-NOV-1993; 93EP-0118993.  
 PR  
 XX 02-DEC-1992; 92DE-4240420.  
 XX  
 PA (FARR) HOECHST AG.  
 XX

PI Gerl M, Ludwig J, Obermeyer R, Sabel W;  
 XX  
 DR WPI: 1994-177718/22.  
 XX  
 PT Prodn. of pro-insulin with correct disulphide bridges - by  
 PT treating recombinant precursor protein with mercaptan in alkali  
 PT and in presence of chaotropic agent, then isolation on  
 PT hydrophobic resin  
 PS  
 XX Disclosure; Page 11; 15pp; German.  
 CC Pro-insulin is produced by treating recombinant precursor protein  
 CC with a mercaptan to provide 2-10 SH residues per Cys residue, in  
 CC presence of a chaotropic agent and in aq. medium of pH 10-11,  
 CC treating the prod. with 3-50 g hydrophobic adsorber resin per 1 g.  
 CC medium of pH 4-7, isolating the adsorbed resin and pro-insulin and  
 CC desorbing the pro-insulin. This method produces pro-insulin with  
 CC correctly bonded Cys bridges. Compared with known methods it  
 CC involves fewer stages (esp. no sulphitolyse or cyanogen bromide  
 CC cleavage) and overall losses during purification are reduced, i.e.  
 CC the process is quicker and gives better yields.  
 CC Sequences of insulin chain A, B and C are given in AAR68895-97.  
 CC Sequences of pro-insulin 1-4 are given in AAR68898-901.  
 CC  
 SQ Sequence 96 AA;  
 Query Match 100.0%; Score 152; DB 15; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 8e-14;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MAPSSSTKKTQLOLEHLDDLQMLINGINN 31  
 DB 1 MAPSSSTKKTQLOLEHLDDLQMLINGINN 31  
 RESULT 6  
 AAR78662 standard; protein; 96 AA.  
 AC AAR78662;  
 XX  
 DT 03-APR-1996 (first entry)  
 XX  
 DE Fusion protein contg. proinsulin sequence 3.  
 XX  
 KM Proinsulin; post-translational modification; recombinant production;  
 KM protein folding; conformation.  
 OS Synthetic.  
 XX  
 OS  
 FT Key Location/Qualifiers  
 FT Region 41..44  
 FT /label= R2  
 FT /note= "a peptide of 4 amino acids"  
 FT 45..74  
 FT /label= R1-(B2-B29)-Y  
 FT /note= "human insulin B-chain"  
 FT 75  
 FT /label= X  
 FT 76..96  
 FT /label= G1Y-(A2-A20)-R3  
 FT /note= "human insulin A-chain"  
 FT  
 PN EP668292-A2.  
 PN  
 XX  
 PD 23-AUG-1995.  
 PF  
 XX 09-FEB-1995; 95EP-0101748.  
 PR  
 XX 18-FEB-1994; 94DE-4405179.  
 XX  
 PA (FARR) HOECHST AG.  
 XX

PI Gerl M, Ludwig J, Obermeier R, Sabel W;  
 XX  
 DR WPI: 1995-284754/38.  
 XX  
 PT Isolation of insulin that is correctly post-translationally  
 PT processed - by reacting pro-insulin with a mercaptan in the presence  
 PT of a chaotropic agent and purification, after absorption to hydrophobic  
 PT resin  
 XX  
 PS Example 2: Page 8: 16pp; German.  
 XX  
 CC The present sequence is that of a fusion protein, produced in E.coli  
 CC which contains an example of a proinsulin molecule corresp.  
 CC to the general formula R2-R1-(B2-B29)-Y-X-Gly-(A2-A20)-R3 (II). In  
 CC formula (II), X = Lys, Arg or a peptide of 2-35 amino acids contg.  
 CC Lys or Arg at the N- and C-termini; Y = a natural amino acid; R1 =  
 CC Phe or a bond; R2 = H, Arg, Lys, a peptide of 2-45 amino acids  
 CC contg. Arg or Lys at the N- and C-termini; R3 = a natural amino  
 CC acid; (A2-A20) and (B2-B29) are the insulin A- and B-chain sequences  
 CC from human or other insulin. The proinsulin molecule, released by  
 CC cyanogen bromide, is reacted with mercaptan at a ratio of 2:10 SH  
 CC residues of mercaptan per Cys residue of proinsulin. The reaction  
 CC takes place in the presence of a chaotropic auxiliary agent at  
 CC pH 10-11 and results in proinsulin with correctly linked B yields  
 CC bridges. Reaction with trypsin and opt. carboxypeptidase B yields  
 CC correctly folded insulin. The insulin is isolated by absorption on  
 CC a hydrophobic resin.  
 CC  
 SO Sequence 96 AA;  
 Query Match 100.0%; Score 152; DB 16; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 8e-14;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MAPSSSTKKTQLOLEHLLDLOMILNGINN 31  
 DB 1 MAPSSSTKKTQLOLEHLLDLOMILNGINN 31  
 RESULT 7  
 AAR22595 AAR22595 standard; Protein: 133 AA.  
 XX  
 AC AAR22595;  
 XX  
 DT 03-NOV-1992 (first entry)  
 XX  
 DE Interleukin-2 used to make hybrid proteins.  
 XX  
 DE IL-2: hybrid; diptheria; toxin; DT; proliferation; peripheral blood;  
 KW mononuclear cells; PBMC; auto-immune response; diabetes; rheumatoid;  
 KW arthritis; allograft rejection; T-suppressor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9206117-A.  
 XX  
 PD 16-APR-1992.  
 XX  
 PF 27-SEP-1991; 91WO-US07342.  
 XX  
 PR 28-SEP-1990; 90US-0590113.  
 XX  
 PA (SERA-) SERAGEN INC.  
 PA (UYHO-) UNIVERSITY HOSPITAL.  
 XX  
 PI Murphy JR, Svrlyuga R;  
 XX  
 DR WPI: 1992-150820/18.  
 DR N-PSDB; AAQ23867.  
 XX  
 PT Hybrid protein comprising portion of the IL-2 binding domain -  
 PT useful for inhibiting unwanted immune responses e.g. autoimmune

PT diseases and reaction to organ and tissue transplants  
 XX  
 PS Disclosure; Fig 1: 37pp; English.  
 XX  
 CC The interleukin-2 protein is part of a hybrid protein comprising  
 CC the binding domain of IL-2 and an enzymatically inactive fragment  
 CC of diptheria toxin which does not include a functional DT  
 CC generalised eukaryotic binding site (see AAR26486). The hybrid  
 CC protein is capable of stimulating the proliferation of peripheral  
 CC blood mononuclear cells in vitro and of suppressing an immune  
 CC response in a mammal in vivo. The hybrid protein allows the  
 CC inhibition of an unwanted immune response such as autoimmune disease,  
 CC e.g. diabetes and rheumatoid arthritis, or allograft rejection. It  
 CC does not cause general immunosuppression, so avoids the resulting  
 CC risk of life threatening infections. In the treatment of allograft  
 CC rejection the hybrid protein spares donor-specific T-suppressor cells,  
 CC which can thus proliferate and aid in prolonging graft survival. The  
 CC hybrid protein does not need to be tailored to individual patients but  
 CC can be used as a universal inhibiting agent. Therapy need not be  
 CC continuous following allograft or an acute stage of autoimmune  
 CC disease, but can be discontinued after a course of treatment.  
 CC  
 SO Sequence 133 AA;  
 Query Match 100.0%; Score 152; DB 13; Length 133;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-13;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MAPSSSTKKTQLOLEHLLDLOMILNGINN 31  
 DB 1 MAPSSSTKKTQLOLEHLLDLOMILNGINN 31  
 RESULT 8  
 AAP40050 AAP40050 standard; Protein: 134 AA.  
 XX  
 AC AAP40050;  
 XX  
 DT 14-JAN-1992 (first entry)  
 XX  
 DE Sequence of an interleukin-2-like polypeptide encoded by the DNA  
 DE insert of PSV-hIL2-O or PSV-hIL2-L.  
 XX  
 DE Diagnosis; therapy; cancer; tumour-specific cytotoxic cell; AIDS;  
 KW multiple sclerosis; lupus; rheumatoid arthritis; herpes;  
 KW viral disease; lymphokine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP118977-A.  
 XX  
 PD 19-SEP-1984.  
 XX  
 PF 25-JAN-1984; 84EP-0300439.  
 XX  
 PR 10-JUN-1983; 83GB-0015981.  
 PR 08-FEB-1983; 83GB-0003383.  
 XX  
 PA (BIOJ ) BIOGEN NV.  
 XX  
 PI Fliers WC, Devos RR;  
 XX  
 DR WPI: 1984-232548/38.  
 DR N-PSDB; AAN40042.  
 XX  
 PT Prodn. of human interleukin 2-like polypeptide(s) - useful  
 PT instead of IL-2 for stimulating the immune system etc.  
 XX  
 PS Claim 6; Page 57-58; 69pp; English.  
 XX  
 CC The DNA sequence is esp. selected from a human chromosomal gene bank,  
 CC e.g. it is a hIL-2 related portion of lambda CH4A-ghIL-2-1 or -2, or

CC of lamda I47-ghIL-2-1, -2 or -3. Transformed hosts are also claimed,  
 CC esp. E.coli, B.spp., B.subtilis, B.stearotherophilus. IL-2-like  
 CC polypeptides are also claimed.

XX Sequence 134 AA:

Query Match 100.0%; Score 152; DB 5; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 1,2e-13;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPTSSSTKKTQLEHLLDLMILGNGINN 31  
 |||  
 DB 1 MAPTSSSTKKTQLEHLLDLMILGNGINN 31

RESULT 9  
 AAP50053  
 ID AAP50053 standard; Protein; 134 AA.

AC AAP50053;

DT 03-SEP-1991 (first entry)

DE Sequence I of new biologically active interleukin 2 (IL-2).

KM Immunological agent; lymphokine.

PN EP163249-A.

XX 04-DEC-1985.

PF 28-MAY-1985; 85EP-0113324.

XX 29-MAY-1984; 84DE-3419995.

PA (FARR) HOECHST AG.

PI Engels J, Uhlmann E, Wengenmayer F, Mullner H, Winnacker EL;

DR Wertz R, Okazaki H;

WIPI: 1985-304738/49.

DR N-PSDB; AAN50037.

PT New biologically active interleukin 2 fragments and derivs. and

PT coding DNA sequences, intermediate oligo-nucleotide(s), hybrid

PT plasmid(s) and transformed cells

PS Disclosure: Page 18-20; 33pp; German.

CC DNA SQs coding for Aas 1-133 and 0-133 (an additional Met) of IL-2  
 CC are claimed, including the CDS of SQ 1 (see AAN50037) with/without 1  
 CC or 2 stop codons. The use of a synthetic gene is esp. convenient  
 CC for expression in E. coli and allows modification of the AA SQ to  
 CC improve peptide stability, solubility or activity. The synthetic  
 CC gene was made from a series of oligonucleotides ligated to form four  
 CC larger fragments designated IL 2-I to 2-IV (see AAN50036).

XX Sequence 134 AA:

Query Match 100.0%; Score 152; DB 6; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 1,2e-13;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPTSSSTKKTQLEHLLDLMILGNGINN 31  
 |||  
 DB 1 MAPTSSSTKKTQLEHLLDLMILGNGINN 31

RESULT 10  
 AAP50855

ID AAP50855 standard; Protein; 134 AA.

XX AAP50855;

XX 01-DEC-1991 (first entry)

DT Sequence encoded by synthetic interleukin II (IL-2) gene.

DE Immunotherapy; lymphokine; interleukin-2; thymocyte mitogenesis.

XX W08500817-A.

PN 28-FEB-1985.

XX 09-AUG-1984; 84WO-US01252.

PF 03-AUG-1984; 84US-0635941.

XX 10-AUG-1983; 83US-0521967.

PA (AMGE-) AMGEN.

PI Souza LM, Stablinsky Y;

DR WPI: 1985-062280/10.

DR N-PSDB; AAN50535.

PT Microbial expression of interleukin II and analogues - by using

PT manufactured DNA sequences to transform microorganisms

XX Example; Table IV, Page 15-16; 39pp; English.

CC The inventors claim a manufactured gene for the prodn. of IL-2 and

CC analogues, and for polypeptides of IL-2 and analogues, and for

CC methods for their recombinant production.

XX Sequence 134 AA:

Query Match 100.0%; Score 152; DB 6; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 1,2e-13;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPTSSSTKKTQLEHLLDLMILGNGINN 31  
 |||  
 DB 1 MAPTSSSTKKTQLEHLLDLMILGNGINN 31

RESULT 11  
 AAP61102  
 ID AAP61102 standard; Protein; 134 AA.

AC AAP61102;

DT 09-MAR-1992 (first entry)

DE Sequence of mature human interleukin 2 (IL2) encoded by SUN-IL2.

XX Yeast expression vector; lymphokine.

OS Homo sapiens.

PN EP171000-A.

PD 12-FEB-1986.

PF 26-JUL-1985; 85EP-0109405.

XX 27-JUL-1984; 84JP-0157038.

PA (SUNR) SUNTORY LTD.

PI Oshima T, Tanaka S, Tsujimoto M, Nakazato H;

XX WPI: 1986-043554/07.

DR N-PSDB; AAN60198.

XX Protein and peptide prodn. by immobilised yeast transformant -





CC 120th, 121st, 123rd, 127th, 129th, 130th, 131st, 132nd and  
 CC 133rd original amino acid residues are replaced by substitution  
 CC amino acid residues. The following 10 analogues of IL-2 are  
 CC specifically claimed: (Cys 8)-', (Gly 47)-', (Cys 80)-',  
 CC (Cys 81)-', (Lys 106)-', (Lys 112)-', (Cys 132)-', (Cys 134)- IL-2.  
 CC Analogues have been constructed to which other molecules can be  
 CC covalently attached without damaging activity. These analogues are used  
 CC to attack toxins, reporter gps. or antiviral or other therapeutic cpds.,  
 CC providing IL-2 conjugates for therapy, or specifically labelled IL-2 for  
 CC development of sensitive biological assays.  
 XX

XX Sequence 134 AA:

Query Match 100.0%; Score 152; DB 11; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAPTSSSTKKTKTQLEHLLDLDLQMTINGINN 31  
 |||  
 DB 1 MAPTSSSTKKTKTQLEHLLDLDLQMTINGINN 31

Search completed: October 25, 2002, 15:48:33  
 Job time : 32 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2002, 15:46:51 ; Search time 13 Seconds  
(without alignments)  
58.246 Million cell updates/sec

Title: US-09-720-828A-2  
Perfect score: 152  
Sequence: 1 MAPSSSTRKTQLEHLLDQMLINGINN 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents,AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	152	100.0	31	4 US-09-116-594-2	Sequence 2, Appli
2	152	100.0	96	1 US-08-160-376A-5	Sequence 5, Appli
3	152	100.0	96	1 US-08-389-487-8	Sequence 8, Appli
4	152	100.0	134	6 5496924-55	Patent No. 5496924
5	147	96.7	50	1 US-08-127-351-13	Sequence 13, Appli
6	147	96.7	50	1 US-08-480-367B-13	Sequence 13, Appli
7	147	96.7	50	1 US-08-487-221A-13	Sequence 13, Appli
8	147	96.7	50	1 US-08-480-370-13	Sequence 13, Appli
9	147	96.7	88	4 US-08-817-787-15	Sequence 15, Appli
10	147	96.7	133	1 US-07-800-366-1	Sequence 1, Appli
11	147	96.7	133	1 US-08-354-456A-5	Sequence 5, Appli
12	147	96.7	133	1 US-08-225-224-3	Sequence 3, Appli
13	147	96.7	133	1 US-08-318-193-89	Sequence 89, Appli
14	147	96.7	133	1 US-08-284-393B-1	Sequence 1, Appli
15	147	96.7	133	1 US-08-284-393B-2	Sequence 1, Appli
16	147	96.7	133	1 US-08-284-393B-3	Sequence 3, Appli
17	147	96.7	133	1 US-08-734-471-1	Sequence 1, Appli
18	147	96.7	133	3 US-08-722-258-3	Sequence 3, Appli
19	147	96.7	133	4 US-08-817-787-13	Sequence 13, Appli
20	147	96.7	133	4 US-09-310-026-1	Sequence 1, Appli
21	147	96.7	133	5 PCT-US95-04468-3	Sequence 3, Appli
22	147	96.7	133	5 PCT-US95-08950-1	Sequence 1, Appli
23	147	96.7	133	5 PCT-US95-08950-2	Sequence 2, Appli
24	147	96.7	133	5 PCT-US95-08950-3	Sequence 3, Appli
25	147	96.7	133	6 5210029-1	Patent No. 5210029
26	147	96.7	133	6 5256769-1	Patent No. 5256769
27	147	96.7	133	6 5464939-2	Patent No. 5464939

28	147	96.7	153	3 US-09-012-366-3	Sequence 3, Appli
29	147	96.7	153	4 US-08-759-628-8	Sequence 8, Appli
30	147	96.7	153	4 US-09-522-217-111	Sequence 111, App
31	147	96.7	153	6 5314995-7	Patent No. 5314995
32	147	96.7	157	4 US-08-818-562-2	Sequence 2, Appli
33	147	96.7	478	3 US-08-155-888-2	Sequence 2, Appli
34	147	96.7	504	1 US-07-932-915-2	Sequence 2, Appli
35	147	96.7	504	1 PCT-US91-05826-2	Sequence 2, Appli
36	144	94.7	251	3 US-08-875-811-59	Sequence 59, Appl
37	144	94.7	254	3 US-08-875-811-61	Sequence 61, Appl
38	143	94.1	133	1 US-08-354-456A-6	Sequence 6, Appli
39	132.5	87.2	127	3 US-08-806-121B-3	Sequence 3, Appli
40	107	70.4	141	4 US-08-930-917A-18	Sequence 18, Appl
41	79	52.0	135	2 US-08-383-621-5	Sequence 5, Appli
42	79	52.0	135	2 US-08-459-906-5	Sequence 5, Appli
43	79	52.0	1098	1 US-07-777-715-7	Sequence 7, Appli
44	79	52.0	1098	1 US-08-170-126-2	Sequence 2, Appli
45	79	52.0	1098	3 US-08-954-418-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-116-594-2  
; Sequence 2, Application US/09116594  
; Patent No. 6168785  
; GENERAL INFORMATION:  
; APPLICANT: THEZE, Jacques  
; APPLICANT: ECKENBERG, Ralph  
; APPLICANT: MOREAU, Jean-Louis  
; APPLICANT: MAZIE, Jean-Claude  
; TITLE OF INVENTION: BIOLOGICAL APPLICATIONS OF NEW PEPTIDES OF IL-2 AND  
; TITLE OF INVENTION: DERIVATIVES AND USE AS THERAPEUTIC AGENTS  
; FILE REFERENCE: 0660-0134-0  
; CURRENT APPLICATION NUMBER: US/09/116,594  
; CURRENT FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide  
US-09-116-594-2  
  
Query Match 100.0%; Score 152; DB 4; Length 31;  
Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 MAPSSSTRKTQLEHLLDQMLINGINN 31  
DB 1 MAPSSSTRKTQLEHLLDQMLINGINN 31  
  
RESULT 2  
US-08-160-376A-5  
; Sequence 5, Application US/08160376A  
; Patent No. 5473049  
; GENERAL INFORMATION:  
; APPLICANT: Obermeier, Ranier  
; APPLICANT: Gerl, Martin  
; APPLICANT: Ludwig, Jurgen  
; APPLICANT: Sabell, Walter  
; TITLE OF INVENTION: Process For Obtaining Proinsulin  
; TITLE OF INVENTION: Possessing Correctly Linked  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenneth A. Genoni, Esq.  
; STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500  
; CITY: Somerville

STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 08876-1258  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 386  
OPERATING SYSTEM: WINDOWS 3.1  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/160,376A  
FILING DATE: December 1, 1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GE P 4240420.7  
FILING DATE: December 2, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Barbara V. Maurer, Esq.  
REGISTRATION NUMBER: 31,287  
REFERENCE/DOCKET NUMBER: HOE 92/F 384  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 231-4079  
TELEFAX: (908) 231-2255  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 Amino Acids  
TYPE: Amino Acid (AA)  
TOPOLOGY: not relevant  
US-08-160-376A-5

Query Match 100.0%; Score 152; DB 1; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.3e-16;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTQLEHLLDQMLNGINN 31  
DB 1 MAPSSSTKKTQLEHLLDQMLNGINN 31

RESULT 3  
US-08-389-487-8  
Sequence 8, Application US/08389487  
Patent No. 5663291  
GENERAL INFORMATION:  
APPLICANT: Obermeier, Rainer  
APPLICANT: Gerl, Martin  
APPLICANT: Ludwig, Jurgen  
APPLICANT: Sabel, Walter  
TITLE OF INVENTION: Process for Obtaining Insulin Having  
TITLE OF INVENTION: Correctly Linked Cystine Bridges  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/389,487  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Einaudi, Carol P.  
REGISTRATION NUMBER: 32,220  
REFERENCE/DOCKET NUMBER: 02481.1424-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-389-487-8

Query Match 100.0%; Score 152; DB 1; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.3e-16;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTQLEHLLDQMLNGINN 31  
DB 1 MAPSSSTKKTQLEHLLDQMLNGINN 31

RESULT 4  
5496924-55  
Patent No. 5496924  
APPLICANT: HABERMANN, PAUL; WENGEMAYER, FRIEDRICH  
TITLE OF INVENTION: FUSION PROTEIN COMPRISING AN  
INTERLEUKIN-2 FRAGMENT BALAST PORTION  
NUMBER OF SEQUENCES: 56  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/194,545  
FILING DATE: 28-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 377,313  
FILING DATE: 10-JUL-1989  
APPLICATION NUMBER: 934,910  
FILING DATE: 25-NOV-1986  
APPLICATION NUMBER: 943,804  
FILING DATE: 19-DEC-1986  
SEQ ID NO: 55  
LENGTH: 134  
5496924-55

Query Match 100.0%; Score 152; DB 6; Length 134;  
Best Local Similarity 100.0%; Pred. No. 2e-16;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTQLEHLLDQMLNGINN 31  
DB 1 MAPSSSTKKTQLEHLLDQMLNGINN 31

RESULT 5  
US-08-127-351-13  
Sequence 13, Application US/08127351  
Patent No. 5449761  
GENERAL INFORMATION:  
APPLICANT: BELINKA JT, BENJAMIN A.  
APPLICANT: COUGHLIN, DANIEL J.  
APPLICANT: ALVAREZ, VERNON L.  
APPLICANT: WOOD, RICHARD  
TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE  
TITLE OF INVENTION: CONSTRUCTS  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER &  
ADDRESS: NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/127,351  
FILING DATE: 28-SEP-1993  
CLASSIFICATION: 534  
ATTORNEY/AGENT INFORMATION:  
NAME: Villacorta, Gilberto M.  
REGISTRATION NUMBER: 34,038  
REFERENCE/DOCKET NUMBER: 4980-004-44  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino/acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-127-351-13

Query Match 96.7%; Score 147; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 3.6e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APTSSSTKKTQLEHLLDLMILNGINN 31  
Db 1 APTSSSTKKTQLEHLLDLMILNGINN 30

RESULT 6  
US-08-480-367B-13  
Sequence 13, Application US/08480367B  
Patent No. 5578268  
GENERAL INFORMATION:  
APPLICANT: BELINKA JR, BENJAMIN A.  
APPLICANT: COUGHLIN, DANIEL J.  
APPLICANT: ALVAREZ, VERNON L.  
APPLICANT: WOOD, RICHARD  
TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE  
TITLE OF INVENTION: CONSTRUCTS  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER  
STREET: 99 Canal Center Plaza, Suite 300  
City: Alexandria  
State: Virginia  
Country: U.S.A.  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,367B  
FILING DATE: 07-06-95  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Villacorta, Gilberto M.  
REGISTRATION NUMBER: 34,038  
REFERENCE/DOCKET NUMBER: 2654-002A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 684-1111  
TELEFAX: (703) 684-1124  
TELEX: - (703) 684-1124  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino/acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

US-08-480-367B-13

Query Match 96.7%; Score 147; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 3.6e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APTSSSTKKTQLEHLLDLMILNGINN 31  
Db 1 APTSSSTKKTQLEHLLDLMILNGINN 30

RESULT 7  
US-08-487-221A-13  
Sequence 13, Application US/08487221A  
Patent No. 5593656  
GENERAL INFORMATION:  
APPLICANT: BELINKA JR, BENJAMIN A.  
APPLICANT: COUGHLIN, DANIEL J.  
APPLICANT: ALVAREZ, VERNON L.  
APPLICANT: WOOD, RICHARD  
TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE  
TITLE OF INVENTION: CONSTRUCTS  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER &  
ADDRESSEE: NEUSTADY, P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
City: Arlington  
State: Virginia  
Country: U.S.A.  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,221A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/127,351  
FILING DATE: 28-SEP-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Villacorta, Gilberto M.  
REGISTRATION NUMBER: 34,038  
REFERENCE/DOCKET NUMBER: 4980-004-44  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino/acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-487-221A-13

Query Match 96.7%; Score 147; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 3.6e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APTSSSTKKTQLEHLLDLMILNGINN 31  
Db 1 APTSSSTKKTQLEHLLDLMILNGINN 30

RESULT 8  
US-08-480-370-13  
Sequence 13, Application US/08480370  
Patent No. 5609847  
GENERAL INFORMATION:

APPLICANT: BELINKA JR, BENJAMIN A.  
APPLICANT: COUGHLIN, DANIEL J.  
APPLICANT: ALVAREZ, VERNON L.  
APPLICANT: WOOD, RICHARD  
TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE  
TITLE OF INVENTION: CONSTRUCTS  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER &  
ADDRESSEE: NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,370  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/127,351  
FILING DATE: 28-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Villacorta, Gilberto M.  
REGISTRATION NUMBER: 34,038  
REFERENCE/DOCKET NUMBER: 4980-004-44  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-480-370-13

Query Match 96.7%; Score 147; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 3.6e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKTKQLQLEHLLDLMILNGINN 31  
DB 1 APTSSSTKTKQLQLEHLLDLMILNGINN 30

RESULT 9  
US-08-817-787-15  
Sequence 15, Application US/08817787  
Patent No. 6294353  
GENERAL INFORMATION:  
APPLICANT: Pack, Peter  
APPLICANT: Lupas, Andrei  
TITLE OF INVENTION: TARGETED HETERO-ASSOCIATION OF  
NUMBER OF SEQUENCES: 36  
TITLE OF INVENTION: RECOMBINANT PROTEINS TO MULTI-FUNCTIONAL COMPLEXES  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,787  
FILING DATE: 23-SEP-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/04117  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94 11 6558.1  
FILING DATE: 20-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 88 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-817-787-15

Query Match 96.7%; Score 147; DB 4; Length 88;  
Best Local Similarity 100.0%; Pred. No. 7.2e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKTKQLQLEHLLDLMILNGINN 31  
DB 3 APTSSSTKTKQLQLEHLLDLMILNGINN 32

RESULT 10  
US-07-800-366-1  
Sequence 1, Application US/07800366  
Patent No. 5250296  
GENERAL INFORMATION:  
APPLICANT: OOTSU, Koichiro  
TITLE OF INVENTION: IMMUNOSTIMULANT AGENT CONTAINING  
NUMBER OF SEQUENCES: 1  
TITLE OF INVENTION: INTERLEUKIN-2 AND 5'-DEOXY-5'-FLUOROURIDINE  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
ADDRESSEE: CUSHMAN  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/800,366  
FILING DATE: 19911127  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Castle, Donald R.  
REGISTRATION NUMBER: 24,220  
REFERENCE/DOCKET NUMBER: 41417(281)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEX: 200281 STRE UR  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids

TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-800-366-1

Query Match 96.7%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLOLEHLLDLOMLNGINN 31  
Db 1 APTSSSTKKTQLOLEHLLDLOMLNGINN 30

RESULT 11  
US-08-354-456A-5  
Sequence 5, Application US/08354456A  
Patent No. 5567611

GENERAL INFORMATION:  
APPLICANT: Ralph, Peter  
APPLICANT: Martin, George  
APPLICANT: Platek, Michael  
APPLICANT: Larrick, James W.  
TITLE OF INVENTION: Multifunctional M-CSF Proteins and Genes Encoding  
TITLE OF INVENTION: Therefor  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: CHIRON CORPORATION  
STREET: Intellectual Property - R440, P.O. Box 8097  
CITY: Emeryville  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/354,456A  
FILING DATE: 12-DEC-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/995,338  
FILING DATE: 21-DEC-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcgarigle Jr., Phillip L.  
REGISTRATION NUMBER: 31,395  
REFERENCE/DOCKET NUMBER: 750,003/32387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2718  
TELEFAX: (510) 655-3542  
TELEX: n/a  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-354-456A-5

Query Match 96.7%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLOLEHLLDLOMLNGINN 31  
Db 1 APTSSSTKKTQLOLEHLLDLOMLNGINN 30

RESULT 12

US-08-225-224-3  
Sequence 3, Application US/08225224  
Patent No. 5635399

GENERAL INFORMATION:  
APPLICANT: PASTAN, Ira  
APPLICANT: KREITMAN, Robert J.  
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND  
TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: Stewart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,224  
FILING DATE: 8-APR-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 15280-193  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FEATURES:  
NAME/KEY: Protein  
LOCATION: 1..133  
OTHER INFORMATION: /label= IL2  
US-08-225-224-3

Query Match 96.7%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLOLEHLLDLOMLNGINN 31  
Db 1 APTSSSTKKTQLOLEHLLDLOMLNGINN 30

RESULT 13  
US-08-318-193-89

Sequence 89, Application US/08318193  
Patent No. 5641663  
GENERAL INFORMATION:  
APPLICANT: GARVIN, Robert T.  
APPLICANT: MALEK, Lawrence T.  
TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION  
TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY  
TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22313-0299

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/318,193  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,314  
FILING DATE:  
APPLICATION NUMBER: US 07/224,568  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 18740/116 CACO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-318-193-89

Query Match 96.7%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDLMILNGINN 31  
DB 1 APTSSSTKKTQLEHLLDLMILNGINN 30

RESULT 14  
US-08-284-393B-1  
Sequence 1, Application US/08284393B  
Patent No. 5696234  
GENERAL INFORMATION:  
APPLICANT: Zurawski, Sandra M.  
TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNA Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/284,393B  
FILING DATE: 01-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0389  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-284-393B-1

Query Match 96.7%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDLMILNGINN 31  
DB 1 APTSSSTKKTQLEHLLDLMILNGINN 30

RESULT 15  
US-08-284-393B-2  
Sequence 2, Application US/08284393B  
Patent No. 5696234  
GENERAL INFORMATION:  
APPLICANT: Zurawski, Sandra M.  
TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNA Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/284,393B  
FILING DATE: 01-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0389  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-284-393B-2

Query Match 96.7%; Score 147; DB 1; Length 133;  
Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDLMILNGINN 31  
DB 1 APTSSSTKKTQLEHLLDLMILNGINN 30

Search completed: October 25, 2002, 15:49:43  
Job time: 15 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2002, 15:48:06 ; Search time 15 Seconds  
(without alignments)  
198.585 Million cell updates/sec

Title: US-09-720-828A-2

Perfect score: 152

Sequence: 1 MAPSSSTRKTKQLQLEHLDDQLQMLINGINN 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR\_71.\*

1: p1r1.\*  
2: p1r2.\*  
3: p1r3.\*  
4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	96.7	153	1	Interleukin-2 prec
2	147	96.7	153	1	Interleukin-2 prec
3	114	75.0	154	2	Interleukin-2 prec
4	97	63.8	155	2	Interleukin-2 prec
5	96	63.2	154	2	Interleukin-2 prec
6	95	62.5	153	2	Interleukin-2 - Mo
7	92	60.5	149	2	Interleukin-2 prec
8	79	52.0	155	2	Interleukin-2 - go
9	79	52.0	155	2	Interleukin-2 prec
10	79	52.0	155	2	Interleukin-2 prec
11	69	45.4	169	2	Interleukin-2 prec
12	64	42.1	169	1	Interleukin-2 prec
13	59.5	39.1	60	2	Interleukin-2 - we
14	58.5	38.5	62	2	Interleukin-2 - we
15	57.5	37.8	72	2	Interleukin-2 - we
16	54	35.5	357	2	Interleukin-2 - we
17	52	34.2	155	1	Interleukin-2 - we
18	52	34.2	155	1	Interleukin-2 - we
19	51	33.6	737	2	Interleukin-2 - we
20	51	33.6	737	2	Interleukin-2 - we
21	50	32.9	627	2	Interleukin-2 - we
22	49	32.2	365	2	Interleukin-2 - we
23	49	32.2	230	2	Interleukin-2 - we
24	49	32.2	543	2	Interleukin-2 - we
25	48.5	31.9	240	2	Interleukin-2 - we
26	48	31.6	441	2	Interleukin-2 - we
27	48	31.6	441	2	Interleukin-2 - we
28	48	31.6	441	2	Interleukin-2 - we
29	48	31.6	1061	1	Interleukin-2 - we

30	47.5	31.2	244	2	T11685	hypothetical prote
31	47.5	31.2	938	2	F86548	polymorphic outer
32	47.5	31.2	938	2	H72074	conserved hypotet
33	47	30.9	398	2	B70209	hypothetical prote
34	47	30.9	557	2	F89839	hypothetical prote
35	47	30.9	1008	2	T41244	SEC14 protein homo
36	47	30.9	1964	2	A53282	nonmuscle myosin I
37	46.5	30.6	159	2	T05656	hypothetical prote
38	46.5	30.6	211	2	C84888	hypothetical prote
39	46.5	30.6	466	2	E90228	amino acid specif
40	46	30.3	293	2	A71946	hypothetical prote
41	46	30.3	323	2	H90434	hypothetical prote
42	46	30.3	380	1	C37760	galactokinase (EC
43	46	30.3	516	2	B64551	oligopeptide ABC t
44	46	30.3	571	2	H82355	peptide ABC transp
45	46	30.3	614	2	T18745	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

Interleukin-2 precursor [validated] - human

N:Alternate names: IL-2; T-cell growth factor

C:Species: Homo sapiens (man)

C:Date: 11-Aug-1983 #sequence\_revision 11-Aug-1983 #text\_change 08-Dec-2000

C:Accession: A01849; A21192; A20961; S31209; A93297; A90113; A53478; I73624;

R:Holbrook, N.J.; Lieber, M.; Crabtree, G.R.

Nucleic Acids Res. 12, 5005-5013, 1984

A:Title: DNA sequence of the 5' flanking region of the human interleukin 2 gene: homo

A:Reference number: A93524; MUID:84247353

A:Accession: A01849

A:Molecule type: DNA

A:Residues: 1-153 <HOL>

A:Cross-references: GB:X00695; GB:X00200; GB:X00201; GB:X00202; NID:g33783; PIDN:CAA2

R:Fujita, T.; Takaoka, C.; Matsui, H.; Taniguchi, T.

Proc. Natl. Acad. Sci. U.S.A. 80, 7437-7441, 1983

A:Title: Structure of the human interleukin 2 gene.

A:Reference number: A21192; MUID:84170243

A:Accession: A21192

A:Molecule type: DNA

A:Residues: 1-153 <Fuj>

A:Cross-references: GB:J00264; NID:g186294; PIDN:AA08509.1; PID:g572676

R:Holbrook, N.J.; Smith, K.A.; Fornace Jr., A.J.; Comeau, C.M.; Wiskocil, R.L.; Crabt

Proc. Natl. Acad. Sci. U.S.A. 81, 1634-1638, 1984

A:Title: T-cell growth factor: complete nucleotide sequence and organization of the g

A:Reference number: A20961; MUID:84170356

A:Accession: A20961

A:Molecule type: DNA

A:Residues: 1-153 <HO2>

A:Cross-references: GB:K02056; NID:g186302; PIDN:AA08792.1; PID:g386819

R:Laibin, Y.; Gress, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapi

EMBO J. 11, 3897-3904, 1992

A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t

A:Reference number: S31206; MUID:93010964

A:Accession: S31206

A:Molecule type: mRNA

A:Residues: 1-117 <LAU>

A:Cross-references: EMBL:Z14955

A:Note: this sequence is shown from the beginning of the fragment to the chromosomal

R:Taniguchi, T.; Matsui, H.; Fujita, T.; Takaoka, C.; Kashima, N.; Yoshimoto, R.; Ham

Nature 302, 305-310, 1983

A:Title: Structure and expression of a cloned cDNA for human interleukin-2.

A:Reference number: A93297; MUID:83167472

A:Accession: A93297

A:Molecule type: mRNA

A:Residues: 1-153 <TAN>

A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781

A:Experimental source: leukemic T-cell line, Jurkat-111, cloned from Jurkat-FHRC

R:Maeda, S.; Nishino, N.; Obaru, K.; Mita, S.; Nomiyama, H.; Shimada, K.; Fujimoto, K

Biochem. Biophys. Res. Commun. 115, 1040-1047, 1983

A:Title: Cloning of interleukin 2 mRNAs from human tonsils.

A:Reference number: A90113; MUID:84023840  
 A:Accession: A90113  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <MAE>  
 A:Cross-references: GB:J00264; NID:9186294; PIDN:AA048509.1; PID:95729676  
 A:Experimental source: tonsillar mononuclear cells  
 R:Devos, R.; Plaeclin, G.; Chevroure, H.; Simons, G.; Degraeve, W.; Tavernier, J.; Remau  
 Nucleic Acids Res. 11, 4307-4323, 1983  
 A:Title: Molecular cloning of human interleukin 2 cDNA and its expression in *Escherichia*  
 A:Reference number: A93478; MUID:83246551  
 A:Accession: A93478  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <DEV>  
 A:Cross-references: GB:V00564; NID:933780; PIDN:CAA3827.1; PID:933781  
 A:Experimental source: splenocytes  
 R:Elzeberg, O.; Faber-Eman, A.; Lotan, M.; Schwartz, M.  
 J. Neurochem. 64, 1928-1936, 1995  
 A:Title: Interleukin-2 transcripts in human and rodent brains: possible expression by as  
 A:Reference number: 156518; MUID:95239150  
 A:Accession: 156518  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-152 <EIZ>  
 A:Cross-references: GB:S77834; NID:9999000  
 A:Accession: 173624  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 5-7, 'F', '9-17', 'P', '19-32', 'X', '34-45', 'X', '47-143' <RES>  
 A:Cross-references: GB:S77835; NID:9999001; PIDN:AA014264.1; PID:94261964  
 R:Nishino, N.; Obaru, K.; Maeda, S.; Shimada, K.; Onoue, K.  
 Biomed. Res. 6, 197-205, 1985  
 A:Title: Organization of the DNA regions flanking the human interleukin 2 gene.  
 A:Reference number: 152528  
 A:Accession: 152528  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-68 <RE2>  
 A:Cross-references: GB:M33199; NID:9186296; PIDN:AA59139.1; PID:9553508  
 R:Stebelnick, U.; Durand, D.B.; Bressler, P.; Holbrook, N.C.; Norris, C.A.; Kamoun, M.;  
 Mol. Cell. Biol. 6, 3042-3049, 1986  
 A:Title: Promoter region of interleukin-2 gene undergoes chromatin structure changes and  
 A:Reference number: 157603; MUID:87064618  
 A:Accession: 157603  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-68 <RE3>  
 A:Cross-references: GB:M13879; NID:9186305; PIDN:AA59141.1; PID:9553509  
 R:Walt, M.P.; Chaplin, M.A.; Wallace, D.M.; Dykes, C.W.; Hobden, A.N.  
 Biochemistry 27, 6883-6892, 1988  
 A:Title: Structure-activity relationships of recombinant human interleukin 2.  
 A:Reference number: 152401; MUID:89062420  
 A:Contents: recombinant IL-2 and mutants expressed in *E. coli*  
 A:Accession: 152401  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 'M', '21-153' <RE4>  
 A:Cross-references: GB:M22005; NID:9186300; PIDN:AA59140.1; PID:9386818  
 A:Note: mutation of Ghe-42 to Ala reduced binding to the IL-2 receptor 5-10 fold without  
 R:Robb, R.J.; Kutny, R.M.; Panico, M.; Morris, H.R.; Chowdhry, V.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 6486-6490, 1984  
 A:Title: Amino acid sequence and post-translational modification of human interleukin 2.  
 A:Reference number: A94009; MUID:85036540  
 A:Accession: A94009  
 A:Molecule type: protein  
 A:Residues: 21-153 <ROB>  
 A:Note: disulfide bonds and carbohydrate binding site were determined  
 A:Note: heterogeneity in Jukat-derived IL-2 is primarily due to differences in glycosyl  
 n in lacking 21-Ala (FT-IL2-A and FT-IL2-B) and 22-Pro (FT-IL2-B)  
 R:Conradt, H.S.; Nimitz, M.; Dittmar, K.E.J.; Lindemaler, W.; Hoppe, J.; Hauser, H.  
 J. Biol. Chem. 264, 17368-17373, 1989  
 A:Title: Expression of human interleukin-2 in recombinant baby hamster kidney, Ltk-, and  
 A:Reference number: A34463; MUID:90008901

A:Accession: A34463  
 A:Molecule type: protein  
 A:Residues: 21-35 <CON>  
 A:Note: the O-linked glycosylation site in recombinant material matched that from hum  
 R:Grabenhorst, E.; Hoyer, B.; Nimitz, M.; Jaeger, V.; Conradt, H.S.  
 Eur. J. Biochem. 215, 189-197, 1993  
 A:Title: Biosynthesis and secretion of human interleukin 2 glycoproteins variants fro  
 A:Reference number: S34052; MUID:93345493  
 A:Contents: annotation; glycosylation of variant forms expressed in insect cells  
 A:Genetics:  
 A:Gene: GDB:IL2  
 A:Cross-references: GDB:119344; OMIM:147680  
 A:Map position: 4q26-4q27  
 A:Introns: 49/3; 69/3; 117/3  
 C:Superfamily: Interleukin-2  
 C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce  
 F:1-20/Domains: signal sequence #status predicted <SIG>  
 F:21-153/Product: Interleukin-2 #status experimental <IL2>  
 F:23/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F:78-125/Disulfide bonds: #status experimental

Query Match 96.7%; Score 147; DB 1; Length 153;  
 Best local Similarity 100.0%; Pred. No. 2e-14;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQQLLEHLLDLQMLNGINN 31  
 DB 21 APTSSSTKKTQQLLEHLLDLQMLNGINN 50

RESULT 2  
 ICG12  
 Interleukin-2 precursor - common gibbon  
 N:Alternate names: IL-2; T-cell growth factor  
 C:Species: Hyllobates lar (common gibbon, white-handed gibbon)  
 C:Date: 31-Dec-1991 #sequence, revision 31-Dec-1991 #text, change 22-Jun-1999  
 C:Accession: A94067; A01849  
 R:Chen, S.J.; Holbrook, N.C.; Mitchell, K.F.; Vallone, C.A.; Greengard, J.S.; Crabtre  
 Proc. Natl. Acad. Sci. U.S.A. 82, 7284-7288, 1985  
 A:Title: A viral long terminal repeat in the interleukin 2 gene of a cell line that c  
 A:Reference number: A94067; MUID:86042650  
 A:Accession: A94067  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <CHE>  
 A:Cross-references: GB:M11144; NID:9177014; PIDN:AA35454.1; PID:9177015  
 A:Experimental source: leukemia cell line M1A 144; ATCC TIB 201  
 A:Note: The integration of a retrovirus sequence containing a 5' LTR into the 3' nonc  
 C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce  
 F:1-20/Domains: signal sequence #status predicted <SIG>  
 F:21-153/Product: Interleukin-2 #status predicted <IL2>  
 F:23/Binding site: carbohydrate (Thr) (covalent) #status predicted  
 F:78-125/Disulfide bonds: #status predicted

Query Match 96.7%; Score 147; DB 1; Length 153;  
 Best local Similarity 100.0%; Pred. No. 2e-14;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQQLLEHLLDLQMLNGINN 31  
 DB 21 APTSSSTKKTQQLLEHLLDLQMLNGINN 50

RESULT 3  
 JN0698  
 Interleukin 2 precursor - cat  
 C:Species: Felis silvestris catus (domestic cat)  
 C:Date: 03-Feb-1994 #sequence, revision 03-Feb-1994 #text, change 16-Jul-1999  
 C:Accession: JN0698  
 R:Cozzoli, P.J.; Padid, P.A.; Takeda, J.; Alegre, M.L.; Yuhki, N.; Leff, A.R.  
 Biochem. Biophys. Res. Commun. 194, 1038-1043, 1993  
 A:Title: Sequence and functional characterization of feline interleukin 2.  
 A:Reference number: JN0698; MUID:93356765



A:Accession: JN0698  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-154 <CO2>  
A:Cross-references: GB:119402; NID:g304313; PIDN:AAA02865.1; PID:g304314  
C:Superfamily: Interleukin-2  
C:Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;  
Best Local Similarity 73.3%; Pred. No. 1.6e-09;  
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLOLEHLLDLOMLGNN 31  
DB 21 APTSSSTKKTQLOLEHLLDLOMLGNN 50

RESULT 4

Interleukin-2 precursor - rat  
N:Alternate names: IL-2; T-cell growth factor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Apr-1989 #sequence\_revision 26-Apr-1989 #text\_change 16-Jul-1999  
C:Accession: A45882; A31278  
R:McKnight, A.J.; Mason, D.W.; Barclay, A.N.  
Immunogenetics 30, 145-147, 1989  
A:Title: Sequence of rat Interleukin 2 and anomalous binding of a mouse Interleukin 2 cDNA  
A:Reference number: A45882; MUID:89339608  
A:Accession: A45882  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <MCK>  
A:Cross-references: GB:M22899; NID:g204909; PIDN:AAA41427.1; PID:g204910  
C:Superfamily: Interleukin-2  
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell

Query Match 63.8%; Score 97; DB 2; Length 155;  
Best Local Similarity 66.7%; Pred. No. 5.6e-07;  
Matches 20; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLOLEHLLDLOMLGNN 31  
DB 21 APTSSSTKKTQLOLEHLLDLOMLGNN 50

RESULT 5

Interleukin-2 precursor - pig  
N:Alternate names: IL-2; T-cell growth factor  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jul-1999  
C:Accession: S16241; S15473  
R:Goodall, J.C.; Emery, D.C.; Bailey, M.; English, L.S.; Hall, L.  
Biochim. Biophys. Acta 1089, 257-258, 1991  
A:Title: cDNA cloning of porcine Interleukin 2 by polymerase chain reaction.  
A:Reference number: S16241; MUID:91274360  
A:Accession: S16241  
A:Molecule type: mRNA  
A:Residues: 1-154 <GOO>  
A:Cross-references: EMBL:X56750; NID:g1991; PIDN:CAA40071.1; PID:g1992

R:Leferve, F.  
submitted to the EMBL Data Library, March 1991  
A:Description: Molecular cloning of porcine Interleukin 2 cDNA by the polymerase chain reaction.  
A:Reference number: S15473  
A:Accession: S15473  
A:Molecule type: mRNA  
A:Residues: 1-154 <LEF>

A:Cross-references: EMBL:X56428; NID:g2068; PIDN:CAA41330.1; PID:g2069  
C:Superfamily: Interleukin-2  
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-154/Product: Interleukin-2 #status predicted <MAT>

Query Match 63.2%; Score 96; DB 2; Length 154;  
Best Local Similarity 66.7%; Pred. No. 7.8e-07;  
Matches 20; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLOLEHLLDLOMLGNN 31  
DB 21 APTSSSTKKTQLOLEHLLDLOMLGNN 50

RESULT 6

Interleukin-2 - Mongolian jird  
S33509  
C:Species: Meriones unguiculatus (Mongolian jird)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Jul-1999  
C:Accession: S33509  
R:Mal, Z.; Klei, T.; Horohov, D.  
submitted to the EMBL Data Library, October 1992  
A:Description: Cross-species PCR cloning of jird (Meriones unguiculatus) Interleukin-2  
A:Reference number: S33509  
A:Accession: S33509  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <MAJ>  
A:Cross-references: EMBL:X68779; NID:g577588; PIDN:CAA48679.1; PID:g311638  
C:Superfamily: Interleukin-2

Query Match 62.5%; Score 95; DB 2; Length 155;  
Best Local Similarity 66.7%; Pred. No. 1.1e-06;  
Matches 20; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLOLEHLLDLOMLGNN 31  
DB 21 APTSSSTKKTQLOLEHLLDLOMLGNN 50

RESULT 7

Interleukin-2 precursor - horse  
S31391  
C:Species: Equus caballus (domestic horse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999  
C:Accession: S31391  
R:Tavernor, A.S.; Butcher, G.W.  
submitted to the EMBL Data Library, November 1992  
A:Description: cDNA cloning of equine Interleukin-2 by polymerase chain reaction.  
A:Reference number: S31391  
A:Accession: S31391  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-149 <TAV>  
A:Cross-references: EMBL:X69393; NID:g1076; PIDN:CAA49190.1; PID:g1077  
C:Superfamily: Interleukin-2

Query Match 60.5%; Score 92; DB 2; Length 149;  
Best Local Similarity 56.7%; Pred. No. 3e-06;  
Matches 17; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLOLEHLLDLOMLGNN 31  
DB 21 APTSSSTKKTQLOLEHLLDLOMLGNN 50

RESULT 8

Interleukin-2 - goat  
S38662  
C:Species: Capra aegagrus hircus (domestic goat)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Jul-1999  
C:Accession: S38662  
R:Rimstad, E.  
submitted to the EMBL Data Library, November 1993  
A:Description: The molecular cloning and expression of caprine Interleukin 2.  
A:Reference number: S38662  
A:Accession: S38662  
A:Status: preliminary

A: Molecule type: mRNA  
A: Residues: 1-155 <RIM>  
A: Cross-references: EMBL: X76063; NID: g416002; PIDD: CAAS3664.1; PIDD: g416003  
C: Superfamily: interleukin-2

Query Match	52.0%;	Score 79;	DB 2;	Length 155;
Best Local Similarity	53.3%;	Pred. No. 0.00027;		
Matches 16; Conservative	6;	Mismatches 8;	Indels 0;	Gaps 0;

```
QY      2 APTSSSTKKTQLQLEHLLDLDMILNGINN 31
          ||||| | :: |||||::: |
Db      21 APTSSSTGNTMKEVKSIILDLQLLLEKVKN 50
```

RESULT 9  
S11488

CISpecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 21-Nov-1993 #sequence, revision 10-Nov-1995 #text\_change 16-Jul-1999  
C:Accession: S11488; S13102; S15517  
R:Goodall J C, Emery D C, Barron A G, P. Macleish J C, Hall J F

A;Title: cdna cloning of ovine interleukin 2 by PCR  
A;Reference number: S11488; MUID:91016933  
A;Accession: S11488

A:status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <GOO>  
A:Cross-references: FMR

A:Title: The molecular cloning of ovine Interleukin 2 gene by the polymerase chain reaction  
R:Shaw, H.F.; Rothel, J.S.; Radford, A.J.; Wood, P.R.  
Nucleic Acids Res. 18, 7175, 1990  
Reference number: S13102; MID:91088336  
Accession number: M13102; EMBL:91088336; FIDN:91088336; FID:91088336

A;Accession: S13102  
A;Status: Preliminary  
A;Molecule type: mRNA  
A;Residues: 1-5, 'L', 7-155 <SEO>

A:Residues:1-5,'L','7-155 <SEO>  
 A:Cross-references: EMBL:X5561; NID:g1810; PIDN:CAA39165.1; PID:g1811  
 R:Buttoso, R.; Williamson, M.L.; Sargan, D.R.; Hahn, W.H.; McConnell, I  
 submitted to the EMBL data Library, April 1991  
 ;Reference number: S15517

A;Accession: S15517  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 21-153 <BUJ>

Query Match 52.0%

OY 2 APTSSSTKKTOLOLEHLLLDLOMILNGINN 31  
 #####  
 Best Local Similarity 53.3%; Pred. No. 0.00027  
 Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

```

Db      21 APTSSSTGNTMKEVKSLLEDLQLLEKVKVN 50
      ||||| | ::: |||||::: | : |
RESULT 10

```

Interleukin-2 precursor - bovine  
C1:Species: Bos primigenius taurus (cattle)  
C1:Date: 16-AUG-1996 #sequence revision 16-AUG-1996 #not changed 16-7-11000

C:\data: 16-Aug-1990 #sequence Revision 16-Aug-1996 #texchange 16-Jul-1999  
C:\Accession: 145913; S21470; S20761  
R.Cerretti, D.P.; McCreghen, K.; Larsen, A.; Cantrell, M.A.; Anderson, D.; Gillis, S.;  
Proc. Natl. Acad. Sci. U.S.A. 83, 3223-3227, 1986  
Title: Cloning, sequencing and expression of bovine interleukin-2

A:Accession: I45913  
A:Reference number: I45913; MUID:86205869  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA

A; Cross-references: GB:M12791. NTD:q163204, P1DN:AAA30586.1; P1D:q163205  
R:Amikheeva, N.N.; Vinogradova, T.V.; Votoshin, O.N.  
A; molecule type: RNA  
A; Residues: 1-155 <CER>

submitted to the EMBL Data Library, December 1989  
A;Reference number: S21470

A:Accession: S21470  
A:Molecule type: DNA  
A:Residues: 1-22 <AN2>  
A:Cross-references: EMBL:X17201; NID:g452; PIDD:CA35062.1; PID:g455

C:Genetics:  
A:Gene: IL-2  
C:Superfamily: Interleukin-2  
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell

Query Match	52.0%;	Score 79;	DB 2;	Length 155;
Best Local Similarity	53.3%;	Pred. No. 0.00027;		
Matches	16;	Conservative	6;	Mismatches 8;
				Indels 0;
				Gaps 0;

```

QY      2 APTSSSTKKTQQLQLEHLDDLDQWILNGINN 31
          ||||| | |:::| |||||:::| | |
Db      21 APTSSSTGNTMKEVKSLLDLDQLLLEKVKV 50

```

RESULT 11  
S37289  
interleuk

```
C:Accession: S37289; S27205; S36162; S24936
R: Todd, J. A.
C: Species: Mus musculus (house mouse)
C: Interactant: p16cds1
C: Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
```

A;Status: preliminary  
A;Accession: S37289  
A;Reference number: S37289  
submitted to the EMBL data library, April 1993

A;Molecule type: mRNA  
A;Residues: 1-169 <TOD>  
A;Cross-references: EMBL  
R;Matesanz, F.; Alcina,

Biochim. Biophys. Acta 1132, 335-336, 1992  
A:Title: A new cDNA sequence for the murine interleukin-2 gene  
A:Reference number: S27205; MJD:93041941  
A:Accession: S27205  
A:Accession number: S27205

A:Residues: 1-63 <MATE>  
A:Molecule type: mRNA  
A:Cross-references: EMBL:X66058, NID:g52725, PIDN:CAA685f.1, PID:g52726  
R:Ghosh, S.; Palmer, S.M.; Rodrigues, N.R.; Cordell, H.J.; Hearne, C.M.; Cornall, R.J.; Gattuso, C. A 404,404, 1002

A:Title: Polygenic control of autoimmune diabetes in nonobese diabetic mice  
A:Reference number: S36162; MID:94004970  
A:Accession: S36162  
A:Status: Preliminary

A;status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-50 <GHO>  
A;Cross-references: EMBL:X73040  
C:Superfamily: interleukin-2

C:Key words: cytokine; glycoprotein; growth factor; lymphokine; T-cell superfamily; interleukin-2  
E:1-20/Domain: signal sequence #status predicted <SIC>  
F:21-63/Product: interleukin-2 #status predicted <MAY>

Query Match 45.4%; Score 69; DB 2; Length 169;  
Best Local Similarity 47.2%; Pred. No. 0.009;  
Matches 17; Conservative 6; Mismatches 7; Indels 6; Gaps 1.

```
QY      2 APTSSSTK7QLQ-----LEHLLDLQMLNGINN 31
          :||||| : | | | | | | | : : |
Db      29 SPTSSSTAFAQQQQQQQHLEQLMDLQELLSRMEN 64
```

RESULT 12  
ICMS2  
interleuk

interleukin-2 precursor - mouse  
N:Alternate names: IL-2; T-cell growth factor (TCGF)  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Jun-1987 #sequence,revision 30-Jun-1987 #text\_change 21-Jul-2000  
C/Accession: A93550; A54490; A94064; I48597; A01850; I84713  
R:Fuse, A.; Fujita, T.; Yasumitsu, H.; Kashima, N.; Hasegawa, K.; Taniguchi, T.

4

Nucleic Acids Res. 12, 9323-9331, 1984  
 A>Title: Organization and structure of the mouse interleukin-2 gene.  
 A:Reference number: A93550; MUID:85087940  
 A:Accession: A93550  
 A:Molecule type: DNA  
 A:Residues: 1-169 <FUS>  
 R:Degrave, W.; Simons, G.; Devos, R.; Plaetnick, G.; Remaut, E.; Tavernier, J.; Fiers, W.  
 Mol. Biol. Rep. 11, 57-61, 1986  
 A>Title: Cloning and structure of a mouse interleukin-2 chromosomal gene.  
 A:Reference number: A54490; MUID:86118396  
 A:Accession: A54490  
 A:Molecule type: DNA  
 A:Residues: 1-169 <DEG>  
 A:Cross-references: GB:M16760  
 R:Yokota, T.; Arai, N.; Lee, F.; Rennick, D.; Mosmann, T.; Arai, K.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 68-72, 1985  
 A>Title: Use of a cDNA expression vector for isolation of mouse interleukin 2 cDNA clone  
 A:Reference number: A94064; MUID:85113172  
 A:Accession: A94064  
 A:Molecule type: mRNA  
 A:Residues: 1-169 <YOK>  
 A:Cross-references: GB:K02292; NID:9198330; PIDN:AAA39289.1; PID:9309404  
 R:Kashima, N.; Nishi-Takaoka, C.; Fujita, T.; Taki, S.; Yamada, G.; Hamuro, J.; Taniguchi  
 Nature 313, 402-404, 1985  
 A>Title: Unique structure of murine interleukin-2 as deduced from cloned cDNAs.  
 A:Reference number: I48597; MUID:85111148  
 A:Accession: I48597  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-169 <RES>  
 A:Cross-references: EMBL:X01772; GB:K02797; NID:952663; PIDN:CAA25909.1; PID:9758159  
 C:Comment: Produced by T-cells in response to antigenic or mitogenic stimulation, this P  
 C:Genetics:  
 A:Introns: 63/3; 83/3; 132/3  
 C:Superfamily: Interleukin-2  
 C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-169/Product: Interleukin-2 #status predicted <MAT>  
 F:23/Binding site: carbohydrate (Thr) (covalent) #status predicted  
 F:92-140/Disulfide bonds: #status predicted

Query Match 42.1%; Score 64; DB 1; Length 169;  
 Best Local Similarity 38.6%; Pred. No. 0.05;  
 Matches 17; Conservative 6; Mismatches 7; Indels 14; Gaps 1;

QY 2 APTSSST-----KKTQLEHLLDQMLINCIN 31  
 :||||| :| | | | | :| :|  
 Db 21 APTSSSTSSSTAFAAQQQQQQQQQHLEQLMDQLSLRMEIN 64

RESULT 13  
 168870  
 Interleukin 2 - western wild mouse (fragment)  
 C:Species: Mus spretus (western wild mouse)  
 C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 16-Jul-1999  
 C:Accession: I68870  
 R:Matessanz, F.; Alcina, A.; Pellicer, A.  
 Immunogenetics 38, 300-303, 1993  
 A>Title: Existence of at least five interleukin-2 molecules in different mouse strains.  
 A:Reference number: I54512; MUID:93307791  
 A:Accession: I68870  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-60 <RES>  
 A:Cross-references: GB:L07575; NID:9349515; PIDN:AAA39327.1; PID:9349516  
 C:Genetics:  
 A:Gene: IL-2  
 C:Superfamily: Interleukin-2

Query Match 39.1%; Score 59.5; DB 2; Length 60;  
 Best Local Similarity 45.5%; Pred. No. 0.072;  
 Matches 15; Conservative 6; Mismatches 5; Indels 7; Gaps 1;

QY 2 APTSSST-----KKTQLEHLLDQMLINCIN 27  
 :||||| :| | | | | :| :|  
 Db 25 APTSSSTSSSTAFAAQQQQQQQHLEQLMDQLSLRMEIN 57

RESULT 14  
 154512  
 Interleukin 2 - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 16-Jul-1999  
 C:Accession: I54512  
 R:Matessanz, F.; Alcina, A.; Pellicer, A.  
 Immunogenetics 38, 300-303, 1993  
 A>Title: Existence of at least five interleukin-2 molecules in different mouse strain  
 A:Reference number: I54512; MUID:93307791  
 A:Accession: I54512  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-62 <RES>  
 A:Cross-references: GB:L07574; NID:9349513; PIDN:AAA39326.1; PID:9349514  
 C:Genetics:  
 A:Gene: IL-2  
 C:Superfamily: Interleukin-2

Query Match 38.5%; Score 58.5; DB 2; Length 62;  
 Best Local Similarity 42.9%; Pred. No. 0.1;  
 Matches 15; Conservative 6; Mismatches 5; Indels 9; Gaps 1;

QY 2 APTSSST-----KKTQLEHLLDQMLINCIN 27  
 :||||| :| | | | | :| :|  
 Db 25 APTSSSTSSSTAFAAQQQQQQQHLEQLMDQLSLRMEIN 59

RESULT 15  
 168871  
 Interleukin 2 - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 16-Jul-1999  
 C:Accession: I68871  
 R:Matessanz, F.; Alcina, A.; Pellicer, A.  
 Immunogenetics 38, 300-303, 1993  
 A>Title: Existence of at least five interleukin-2 molecules in different mouse strain  
 A:Reference number: I54512; MUID:93307791  
 A:Accession: I68871  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-72 <RES>  
 A:Cross-references: GB:L07576; NID:9349517; PIDN:AAA39328.1; PID:9349518  
 C:Genetics:  
 A:Gene: IL-2  
 C:Superfamily: Interleukin-2

Query Match 37.8%; Score 57.5; DB 2; Length 72;  
 Best Local Similarity 35.6%; Pred. No. 0.18;  
 Matches 16; Conservative 5; Mismatches 5; Indels 19; Gaps 1;

QY 2 APTSSSTKKTQLEHLLDQMLINCIN 27  
 :||||| :| | | | | :| :|  
 Db 25 APTSSSTSSSTAFAAQQQQQQQHLEQLMDQLSLRMEIN 69

Search completed: October 25, 2002, 15:50:06  
 Job time : 17 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2002, 15:44:15 ; Search time 11 Seconds  
(without alignments)  
109.119 Million cell updates/sec

Title: US-09-720-828a-2

Perfect score: 152

Sequence: 1 MAPTSSSTKKTQLQLFHLLDLQMLINGINN 31

Scoring table: BLASTSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	147	96.7	153	1 IL2_HUMAN	P01585 homo sapien
2	147	96.7	154	1 IL2_MACFA	O29615 macaca fasc
3	147	96.7	154	1 IL2_MACMU	P14498 macaca mula
4	142	93.4	154	1 IL2_CERVO	P46649 cervocobus
5	116	76.3	154	1 IL2_MIRAN	O62641 mirounga an
6	114	75.0	154	1 IL2_FELCA	O07885 felis silve
7	107.5	70.7	153	1 IL2_CANFA	O29416 canis famli
8	107	70.4	153	1 IL2_RABIT	O77620 oryctolagus
9	97	63.8	155	1 IL2_RAT	P17108 rattus norv
10	96	63.2	154	1 IL2_PIG	P26891 sus scrofa
11	95	62.5	155	1 IL2_MERUN	O08081 meriones un
12	92	60.5	149	1 IL2_HORSE	P37997 equus cabal
13	88	57.9	152	1 IL2_ORCOR	O97513 orclinus orc
14	79	52.0	155	1 IL2_BOVIN	P05016 bos taurus
15	79	52.0	155	1 IL2_CAPIH	P36835 capra hircu
16	79	52.0	155	1 IL2_SHEEP	P19114 ovis aries
17	79	52.0	155	1 IL2_SHEEP	P19114 ovis aries
18	64.5	42.4	162	1 IL2_CEREL	P51747 cervus elap
19	64	42.1	169	1 IL2_MUSSP	O08867 mus spretus
20	54	35.5	137	1 AAAA_EMENT	P04351 mus musculu
21	52	34.2	155	1 YHCH_HAINT	P21133 emeritella
22	51	33.6	167	1 FLGK_BORBU	P44588 haemophilus
23	50	32.9	1046	1 POL_SIVAG	P70780 simian immu
24	48	31.6	189	1 Y064_MERJA	P27980 simian immu
25	47.5	31.2	1061	1 POL_SIVAT	O60376 methanococc
26	46	30.3	293	1 PM15_CHLPT	O05895 simian immu
27	46	30.3	293	1 Y347_HELPJ	O92883 chlamydia p
28	46	30.3	627	1 YHA8_YEAST	O92883 chlamydia p
29	46	30.3	715	1 LCCL_LACIA	P28750 saccharomyc
30	46	30.3	1403	1 PRO_DROME	O9C1B8 lactococcus
31	46	30.3	1612	1 DNMI_PARLI	P29617 diptophylla
32	45	29.6	1	1 A85C_MYCLE	O27746 paracaterot
33	45	29.6	715	1 LCNC_LACIA	O05865 mycobacteri

34	45	29.6	870	1	P01_JSRV	P31623 sheep pulmo
35	45	29.6	903	1	MSPI_SCHPO	P87320 schizosacch
36	45	29.6	1158	1	ALAI_ARATH	P98204 arabidopsi
37	44.5	29.3	511	1	DOPI_DROME	P41596 drosophila
38	44.5	29.3	741	1	RNSA_HUMAN	O05823 homo sapien
39	44	28.9	81	1	EXTS_PASMO	O9C8A0 pasteurella
40	44	28.9	357	1	CAD4_TOBAC	P30359 nicotiana t
41	44	28.9	357	1	CAD9_TOBAC	P30360 nicotiana t
42	44	28.9	368	1	LEU3_NEUCR	P34738 neurospora
43	44	28.9	474	1	SYPA_ARCFU	O28324 archaeoglob
44	44	28.9	625	1	XYNA_PIRSP	O12667 plasmocys s
45	44	28.9	943	1	YLM5_CAEEL	P34408 caenorhabdi

# ALIGNMENTS

RESULT 1	IL2_HUMAN	STANDARD:	PRT:	153	AA.
AC	P01585;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)				
DE	(Aldelesleukin).				
GN	IL2.				
OS	Homo sapiens (Human), and				
OS	Hylobates lar (Common gibbon).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID:9606, 9580;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-Human;				
RX	MEDLINE=84247353; PubMed=6330695;				
RA	Holbrook N.J., Lieber M., Crabtree G.R.;				
RT	"DNA sequence of the 5' flanking region of the human Interleukin 2				
RT	gene: homologues with adult T-cell leukemia virus.";				
RL	Nucleic Acids Res. 12:5005-5013(1984).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-Human;				
RX	MEDLINE=83167472; PubMed=6403867;				
RA	Taniguchi T., Matsui H., Fujita T., Takaoka C., Kashima N.,				
RA	Yoshimoto R., Hamuro J.;				
RT	"Structure and expression of a cloned cDNA for human Interleukin-2.";				
RL	Nature 302:305-310(1983).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-Human;				
RX	MEDLINE=84023840; PubMed=6312994;				
RA	Maeda S., Nishino N., Obaru K., Mita S., Nomiyama H., Shinada K.,				
RA	Fujimoto K., Teranishi T., Hirano T., Onoue K.;				
RT	"Cloning of Interleukin 2 mRNAs from human tonsils.";				
RL	Biochem. Biophys. Res. Commun. 115:1040-1047(1983).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-Human;				
RX	MEDLINE=83246551; PubMed=6306584;				
RA	Devos R., Plactinck G., Cheroutre H., Simons G., Degraeve W.,				
RA	Tavernier J., Remaut E., Fiers W.;				
RT	"Molecular cloning of human Interleukin 2 cDNA and its expression in				
RT	E. coli.";				
RL	Nucleic Acids Res. 11:4307-4323(1983).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES-Human;				
RX	MEDLINE=84170356; PubMed=6608729;				
RA	Holbrook N.J., Smith K.A., Fornace A.J. Jr., Comeau C.M.,				
RA	Wiskocil R.L., Crabtree G.R.;				
RT	"T-cell growth factor: complete nucleotide sequence and organization				
RT	of the gene in normal and malignant cells.";				

RL Proc. Natl. Acad. Sci. U.S.A. 81:1634-1638(1984).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-Human:  
 RX MEDLINE=84170243; PubMed=6324170;  
 RA Fujita T., Takeoka C., Matsui H., Taniguchi T.;  
 RT "Structure of the human interleukin 2 gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:7437-7441(1983).  
 RN [17]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-Human:  
 RX MEDLINE=95239150; PubMed=7722480;  
 RA Eisenberg O., Faber-Elman A., Lotan M., Schwartz M.;  
 RT "Interleukin-2 transcripts in human and rodent brains: possible  
 expression by astrocytes.";  
 RL J. Neurochem. 64:1928-1936(1995).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-Human:  
 RX MEDLINE=96422299; PubMed=8824916;  
 RA Chernicky C.L., Tan H., Burfield P., Ilan J., Ilan J.;  
 RT "Sequence of interleukin-2 isolated from human placental poly A+ RNA:  
 possible role in maintenance of fetal allograft.";  
 RL Mol. Reprod. Dev. 43:180-186(1996).  
 RN [9]  
 RP SEQUENCE OF 21-153 FROM N.A.  
 RC SPECIES-Human:  
 RX MEDLINE=89062420; PubMed=3264184;  
 RA Weir M.P., Chaplin M.A., Wallace D.M., Dykes C.W., Hobden A.N.;  
 RT "Structure-activity relationships of recombinant human interleukin  
 2.";  
 RL Biochemistry 27:6883-6892(1988).  
 RN [10]  
 RP SEQUENCE OF 1-69 FROM N.A.  
 RC SPECIES-Human:  
 RX MEDLINE=87064618; PubMed=3491296;  
 RA Siebenlist U., Durand D.B., Bressler P., Holbrook N.J., Norris C.A.,  
 RA Kamoun M., Kant J.A., Crabtree G.R.;  
 RT "Promoter region of interleukin-2 gene undergoes chromatin structure  
 changes and confers inducibility on chloramphenicol acetyltransferase  
 gene during activation of T cells.";  
 RL Mol. Cell. Biol. 6:3042-3049(1986).  
 RN [11]  
 RP SEQUENCE OF 1-68 FROM N.A.  
 RC SPECIES-Human:  
 RX Nishino N., Obari K., Maeda S., Shimada K., Onoue K.;  
 RT "Organization of the DNA regions flanking the human interleukin 2  
 gene.";  
 RL Biomed. Res. 6:197-205(1985).  
 RN [12]  
 RP SEQUENCE OF 21-153, DISULFIDE BOND, AND CARBOHYDRATE-LINKAGE SITE.  
 RC SPECIES-Human:  
 RX MEDLINE=85038540; PubMed=6333684;  
 RA Robb R.J., Kutny R.M., Panico M., Morris H.R., Chowdhry V.;  
 RT "Amino acid sequence and post-translational modification of human  
 interleukin 2.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:6486-6490(1984).  
 RN [13]  
 RP CARBOHYDRATE-LINKAGE SITE.  
 RC SPECIES-Human:  
 RX MEDLINE=9008901; PubMed=2793860;  
 RA Conradt H.S., Nlntz M., Diltmar K.E.J., Lindenmeyer W., Hoppe J.,  
 HAUSER H.;  
 RT "Expression of human interleukin-2 in recombinant baby hamster  
 kidney, Ltk-, and Chinese hamster ovary cells. Structure of O-linked  
 carbohydrate chains and their location within the polypeptide.";  
 RL J. Biol. Chem. 264:17368-17373(1989).  
 RN [14]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-H. lar:  
 RX MEDLINE=86042650; PubMed=3877307;  
 RA Chen S.J., Holbrook N.J., Mitchell K.F., Vallone C.A.,  
 RA Greengard J.S., Crabtree G.R., Lin Y.;

RT "A viral long terminal repeat in the interleukin 2 gene of a cell  
 line that constitutively produces interleukin 2.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7284-7288(1985).  
 RN [15]  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
 RC SPECIES-Human:  
 RX MEDLINE=88070646; PubMed=3500515;  
 RA Brandhuber B.J., Boone F., Kenney W.C., McKay D.B.;  
 RT "Three-dimensional structure of interleukin-2.";  
 RL Science 238:1707-1709(1987).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=92335891; PubMed=1631562;  
 RA Bazan J.F.;  
 RT "Unraveling the structure of IL-2.";  
 RL Science 257:410-412(1992).  
 RN [17]  
 RP RESPONSE TO ABOVE LETTER.  
 RA McKay D.B.;  
 RL Science 257:412-413(1992).  
 RN [18]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=92379010; PubMed=1510960;  
 RA Molt H.R., Driscoll P.C., Boyd J., Cooke R.M., Weir M.P.,  
 RA Campbell I.D.;  
 RT "Secondary structure of human interleukin 2 from 3D heteronuclear NMR  
 experiments.";  
 RL Biochemistry 31:7741-7744(1992).  
 RN [19]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE=9511955; PubMed=7529123;  
 RA Bamorough P., Hedgecock C.J., Richards W.G.;  
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular  
 modelling.";  
 RL Structure 2:839-851(1994).  
 CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
 MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL  
 PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE  
 IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-  
 ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS  
 CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)  
 WHICH INVOLVES IL2 AND BCMA.  
 CC -1- PHARMACEUTICAL: Available under the name Proleukin (Chiron). Used  
 in patients with renal cell carcinoma or metastatic melanoma.  
 CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
 CC -1- DATABASE: NAME-RKD systems' cytokine source book: IL2;  
 WWW="http://www.rndsyste.ms.com/asp/g\_sitebuilder.asp?bodyId=206".  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: J00264; AAD48509.1; -  
 DR EMBL: X01586; CAA25742.1; -  
 DR EMBL: V00564; CAA23827.1; -  
 DR EMBL: X00695; CAA25292.1; -  
 DR EMBL: R02056; AAA98792.1; -  
 DR EMBL: M13879; AAA59141.1; -  
 DR EMBL: K03174; AAA35453.1; -  
 DR EMBL: S77834; AAD14263.2; -  
 DR EMBL: S82692; AAB46883.1; -  
 DR EMBL: M22005; AAA59140.1; -  
 DR EMBL: M11144; AAA35454.1; -  
 DR EMBL: M33199; AAA59138.1; -  
 DR EMBL: A14844; CAA01199.1; -  
 DR PIR: A01849; ICH02.  
 DR PIR: A94067; ICG12.

```

Query Match      96.7%: Score 147; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLOLEHLLDLOMILNGINN 31
Db 21 APTSSSTKKTQLOLEHLLDLOMILNGINN 50

RESULT 2
IL2_MACFA
ID IL2_MACFA STANDARD; PRT; 154 AA.
AC Q29615;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_Taxid=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Yabe M., Matsura Y., Tatsumi M.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION. THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D63352; BAA09676.1; -.
DR HSSP; P01585; 3INX.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
KM SIGNAL.
FT CHAIN 1 20 BY SIMILARITY.
FT CARBOHYD 21 154 INTERLEUKIN-2.
FT DISULFID 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT SEQUENCE 78 126 BY SIMILARITY.
SO SEQUENCE 154 AA; 17686 MW; 7853FE624A5E4A9 CRC64;

Query Match      96.7%: Score 147; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLOLEHLLDLOMILNGINN 31
Db 21 APTSSSTKKTQLOLEHLLDLOMILNGINN 50

RESULT 3
IL2_MACMU

```

```

ID IL2_MACMU STANDARD; PRT; 154 AA.
AC P51498;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Macaca mulatta (Rhesus macaque), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_Taxid=9544, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikxala N., Ansari A.A.;
RT *Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.
RL J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION. THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U19847; AAB60400.1; -.
DR EMBL; U19852; AAB6714.1; -.
DR HSSP; P01585; 3INX.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
KM SIGNAL.
FT CHAIN 1 20 BY SIMILARITY.
FT CARBOHYD 21 154 INTERLEUKIN-2.
FT DISULFID 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT SEQUENCE 78 126 BY SIMILARITY.
SO SEQUENCE 154 AA; 17685 MW; 6AEB4A80F204BA49 CRC64;

Query Match      96.7%: Score 147; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLOLEHLLDLOMILNGINN 31
Db 21 APTSSSTKKTQLOLEHLLDLOMILNGINN 50

RESULT 4
IL2_CERTO
ID IL2_CERTO STANDARD; PRT; 154 AA.
AC P46649;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.

```

```

OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA MEDLINE=66003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikala N., Ansari A.A.;
RT *Comparative sequence analysis of cytokine genes from human and
nonhuman primates.
RL J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U19846; AAB60399.1; -.
DR HSSP: P01585; 3INK.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam: PF00715; IL2; 1.
DR PRINTS: PR00265; INTERLEUKIN2.
DR ProDom: PD003649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
DR PROSITE: PS00424; INTERLEUKIN_2; 1.
DR PROSITE: PS00424; INTERLEUKIN_2; 1.
DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
FT VARIANT 25 25 R -> S.
FT VARIANT 74 74 K -> E.
SQ SEQUENCE 154 AA; 17754 MW; 9EB51814204BA8 CRC64;

Query Match 93.4%; Score 142; DB 1; Length 154;
Best Local Similarity 96.7%; Pred. No. 2e-14;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDMLINGINN 31
DB 21 APTSSSTKKTQLEHLLDMLINGINN 50

RESULT 5
IL2_MIRAN STANDARD; PRT; 154 AA.
AC 06264;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Mirounga angustirostris (Northern elephant seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Plinnipedia; Phocidae; Mirounga.
OX NCBI_TaxID=9716;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98136706; PubMed=9476229;
RA Shoda L.K.M., Brown W.C., Rice-Ficht A.C.;

```

```

RT *Sequence and characterization of feline interleukin 2."
RL J. Wildl. Dis. 34:81-90(1998).
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U79187; AAC12258.1; -.
DR HSSP: P01585; 3INK.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam: PF00715; IL2; 1.
DR PRINTS: PR00265; INTERLEUKIN2.
DR ProDom: PD003649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
DR PROSITE: PS00424; INTERLEUKIN_2; 1.
DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
SQ SEQUENCE 154 AA; 17661 MW; 0C92337A4B166BB CRC64;

Query Match 76.3%; Score 116; DB 1; Length 154;
Best Local Similarity 73.3%; Pred. No. 1.7e-10;
Matches 22; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDMLINGINN 31
DB 21 APTSSSTKKTQLEHLLDMLINGINN 50

RESULT 6
IL2_FELCA STANDARD; PRT; 154 AA.
AC 007885;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93356765; PubMed=8352761;
RA Cozzi P.J., Padrid P.A., Takeda J., Alegre M.-A., Yuhki N.,
RA Left A.R.;
RT *Sequence and functional characterization of feline interleukin 2."
RL Blochem. Biophys. Res. Commun. 194:1038-1043(1993).
RN [2]
RN SEQUENCE FROM N.A.
RA Litman R., Gibbs C., Good R.A., Day N.K.;
RA Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.

```



CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: L19402; AAA02865.1; -;  
 CC EMBL: L25408; AAA51431.1; -;  
 CC PIR: JN0698; JN0698.  
 CC HSSP: P01585; 3INK.  
 CC InterPro: IPR000779; Interleukin-2.  
 CC Pfam: PF00715; IL2; 1.  
 CC PRINTS: PR00265; INTERLEUKIN2.  
 CC PRODOM: PD003649; Interleukin-2; 1.  
 CC SMART: SM00189; IL2; 1.  
 CC PROSITE: PS00424; INTERLEUKIN-2; 1.  
 CC CytoKine; Glycoprotein; Immune response; Signal; Growth factor;  
 CC T-cell.  
 KW SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 154 INTERLEUKIN-2.  
 FT DISULFID 78 126 BY SIMILARITY.  
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 3 4 KI -> RM (IN REF. 2).  
 FT CONFLICT 150 150 F -> I (IN REF. 2).  
 SQ SEQUENCE 154 AA; 17653 MW; 2E71E3BDB89665EF CRC64;  
 Query Match 75.0%; Score 114; DB 1; Length 154;  
 Best Local Similarity 73.3%; Pred. No. 3.4e-10;  
 Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 APTSSSTKKTQLEHLDDLQMLINGINN 31  
 DB 21 APASSSTKETQOLEQLLDLQLLNGVNN 50  
 RESULT 7  
 IL2\_CANFA STANDARD; PRT; 155 AA.  
 AC Q29416; Q29416;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN IL2.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OC NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=XBRED21/12/93; TISSUE=lymph node;  
 RX MEDLINE=95337423; PubMed=7612930;  
 RA Dunham S.P., Argyle D.J., Onions D.E.;  
 RT "The isolation and sequence of canine Interleukin-2";  
 RL DNA Seq. 5:177-180(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=96016696; PubMed=8571541;  
 RA Somborg R.L., Pullen R.P., Casel M.L., Patterson D.F., Felsburg P.J.,  
 RA Henthorn P.S.;  
 RT "A single nucleotide insertion in the canine interleukin-2 receptor  
 RT gamma chain results in x-linked severe combined immunodeficiency  
 RT disease";  
 RL Vet. Immunol. Immunopathol. 47:203-213(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=BEAGLE; TISSUE=Spleen;  
 RX MEDLINE=95347614; PubMed=7622066;

RA Knapp D.W., Williams J.S., Andrisani O.M.;  
 RT "Cloning of the canine Interleukin-2-encoding cDNA";  
 RL Gene 159:281-282(1995).  
 CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
 CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL  
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE  
 CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-  
 CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: D30710; BAA06378.1; -;  
 CC EMBL: U28141; AAA68969.1; -;  
 CC EMBL: U11689; AAA75360.1; -;  
 CC HSSP: P01585; 3INK.  
 CC InterPro: IPR000779; Interleukin-2.  
 CC Pfam: PF00715; IL2; 1.  
 CC PRINTS: PR00265; INTERLEUKIN2.  
 CC PRODOM: PD003649; Interleukin-2; 1.  
 CC SMART: SM00189; IL2; 1.  
 CC PROSITE: PS00424; INTERLEUKIN-2; 1.  
 CC CytoKine; Glycoprotein; Immune response; Signal; Growth factor;  
 CC T-cell.  
 KW SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 155 INTERLEUKIN-2.  
 FT CARBOHYD 24 24 O-LINKED (GALNAC. . .) (BY SIMILARITY).  
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 79 127 BY SIMILARITY.  
 FT CONFLICT 4 4 M -> I (IN REF. 3).  
 FT CONFLICT 37 37 Q -> R (IN REF. 3).  
 FT CONFLICT 151 151 F -> Y (IN REF. 3).  
 FT CONFLICT 154 154 L -> M (IN REF. 3).  
 SQ SEQUENCE 155 AA; 17668 MW; D123E486B7F4ACID CRC64;  
 Query Match 70.7%; Score 107.5; DB 1; Length 155;  
 Best Local Similarity 71.0%; Pred. No. 3.3e-09;  
 Matches 22; Conservative 6; Mismatches 2; Indels 1; Gaps 1;  
 QY 2 APTSSSTKKTQLEHLDDLQMLINGINN 31  
 DB 21 APTSSSTKETQOLEQLLDLQLLNGVNN 51  
 RESULT 8  
 IL2\_RABIT STANDARD; PRT; 153 AA.  
 AC Q77620;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN IL2.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OC NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Lymph node;  
 RA Kerr P.J., Lei S., Hardy C., Perkins H.D.;  
 RT "Complete cDNA sequence of rabbit interleukin-2";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR  
 CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL  
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE



DR EMBL; X68779; CAA486  
DR PIR; S33509; S33509.  
DR HSSP; P01585; 3INK.

DR SMART; SM00189; IL2; 1.  
DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor

```

FT CHAIN 21 >152 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNLC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
FT NON_TER 152 152
SQ SEQUENCE 152 AA; 17424 MW; 308FP91821BCB764 CRC64;

Query Match 57.9%; Score 88; DB 1; length 152;
Best Local Similarity 60.0%; Pred. No. 2.9e-06;
Matches 18; Conservative 6; Mismatches 6; Indels 0; Gaps 0

QY 2 APPSSSTKKTQLQLLEHLILDQNLINGINN 31
Db 21 APTSSSTENTKKOVOSIIDLQILLKEINN 50
||||| : : : ||| : |||

RESULT 14
IL2_BOVIN STANDARD; PRT; 155 AA.
ID IL2_BOVIN
AC P05016;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DI Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2 OR IL-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86205869; PubMed=3517854;
RA Cerretti D.P., McKereghan K., Larsen A., Cantrell M.A., Anderson D.,
RA Gillis S., Cosman D., Baker P. E.;
RT "Cloning, sequence, and expression of bovine interleukin 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3223-3227(1986).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86205870; PubMed=3486415;
RA Reeves R., Spies A.G., Nissen M.S., Buck C.D., Weinberg A.D.,
RA Barr P.J., Magnuson N.S., Magnuson J.A.;
RT "Molecular cloning of a functional bovine interleukin 2 cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3228-3232(1986).
[3]
RP SEQUENCE OF 1-22 FROM N.A.
RA TISSUE=Thymus;
RC Anikeeva N.N., Vinogradova T.V., Voloshin O.N.;
RL Submitted (DEC-1989) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION. THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC
DR EMBL: M12791; AAA30586.1; -
DR EMBL: M13204; AAA21143.1; ALT_INIT.
DR EMBL: X17201; CAA35062.1; -
DR EMBL: X52687; CAA36912.1; -
DR HSSP: P01585; 31NK.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam: PF00715; IL2; 1.
DR PRINTS: PR00265; INTERLEUKIN2.
DR ProDom: PD003649; INTERLEUKIN-2; 1

```

```

DR SMART: SM00189; IL2; 1.
DR PROSITE: PS00424; INTERLEUKIN_2; 1.
KM Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KM T-cell.
FT SIGNAL 1 20
FT CHAIN 21 155 INTERLEUKIN-2.
FT DISULFID 79 127 BY SIMILARITY.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT CONFLICT 66 66 V -> A (IN REF. 2).
SQ SEQUENCE 155 AA; 17627 MW; 816667DFA052EDF CRC64;

Query Match 52.0%; Score 79; DB 1; Length 155;
Best Local Similarity 53.3%; Pred. No. 6.7e-05;
Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLOLEHLLDLOMLNGINN 31
DB 21 APTSSSTGNTMKVEKSLLDLDLLEKVN 50

RESULT 15
IL2_CAPRI STANDARD; PRT; 155 AA.
AC P36835; P79156;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Rimstad E.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC Beyer J.C., Cheevers W.P.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X76063; CAAS3664.1; -.
CC DR EMBL: U34274; AAB38527.1; -.
CC DR PIR: S38662; S38662.
CC DR HSP: P01585; 31NK.
CC DR InterPro: IPR000779; Interleukin-2.
CC DR Pfam: PF00715; IL2; 1.
CC DR PRINTS: PR00265; INTERLEUKIN2.
CC DR PRODOM: PD003649; Interleukin-2; 1.
CC DR SMART: SM00189; IL2; 1.
CC DR PROSITE: PS00424; INTERLEUKIN_2; 1.
CC CYCLOP: Glycoprotein; Immune response; Signal; Growth factor;.
KM T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 155 INTERLEUKIN-2.

```

```

FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 79 127 BY SIMILARITY.
FT CONFLICT 3 5 RMQ -> QIP (IN REF. 2).
FT CONFLICT 22 22 P -> T (IN REF. 2).
FT CONFLICT 30 30 T -> P (IN REF. 2).
FT CONFLICT 51 51 L -> P (IN REF. 2).
FT CONFLICT 71 71 D -> A (IN REF. 2).
FT CONFLICT 89 89 D -> E (IN REF. 2).
FT CONFLICT 99 99 R -> L (IN REF. 2).
FT CONFLICT 107 113 YMASLG -> SMDNIKR (IN REF. 2).
FT CONFLICT 140 140 O -> L (IN REF. 2).
FT CONFLICT 144 144 T -> I (IN REF. 2).
FT CONFLICT 154 154 L -> M (IN REF. 2).
SQ SEQUENCE 155 AA; 17703 MW; 90022DFB6AF78DF CRC64;

Query Match 52.0%; Score 79; DB 1; Length 155;
Best Local Similarity 53.3%; Pred. No. 6.7e-05;
Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLOLEHLLDLOMLNGINN 31
DB 21 APTSSSTGNTMKVEKSLLDLDLLEKVN 50

```

Search completed: October 25, 2002, 15:48:51  
 Job time : 13 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: October 25, 2002, 15:44:41 ; Search time 25 Seconds  
(without alignments)  
214.514 Million cell updates/sec

Title: US-09-720-828A-2

Perfect score: 152  
Sequence: 1 MAPTSSSTKKTQQLQLEHLLDLQMLINGINN 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

SPREMBL\_19:\*

- 1: SP\_Archaea:\*
- 2: SP\_Bacteria:\*
- 3: SP\_Fungi:\*
- 4: SP\_Human:\*
- 5: SP\_Invertebrate:\*
- 6: SP\_Mammal:\*
- 7: SP\_Mhc:\*
- 8: SP\_Organelle:\*
- 9: SP\_Phage:\*
- 10: SP\_Plant:\*
- 11: SP\_Rodent:\*
- 12: SP\_Virus:\*
- 13: SP\_Vertebrate:\*
- 14: SP\_Unclassified:\*
- 15: SP\_Virus:\*
- 16: SP\_Bacteriap:\*
- 17: SP\_Archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	96.7	150	4	09C001
2	145	95.4	154	6	09XS38
3	135.5	89.1	156	4	013169
4	134	88.2	139	4	016334
5	108.5	71.4	155	6	09XT83
6	107.5	70.7	66	6	09BG74
7	107	70.4	79	6	09TV12
8	106	69.7	133	6	09MZ89
9	105	69.7	155	11	09Z3T2
10	103	67.8	138	11	0703Z9
11	91	59.9	23	4	09UCF5
12	83	54.6	154	6	09XT84
13	82	53.9	152	11	088210
14	79	52.0	69	6	09GJR4
15	79	52.0	155	6	09GL83
16	79	52.0	155	6	095MP4

17	79	52.0	155	6	095KP3	095kp3 bubalus bub
18	69	45.4	39	6	09BG73	09bg73 canis fam11
19	69	45.4	150	11	P70291	P70291 mus musculu
20	69	45.4	169	11	09QUS8	09qus8 mus musculu
21	67	44.1	150	11	P70294	P70294 mus musculu
22	65.5	43.1	155	11	P70292	P70292 mus musculu
23	62.5	41.1	159	11	P70293	P70293 mus musculu
24	52	34.2	116	6	029138	029138 trichechus
25	52	34.2	737	16	09KTG5	09ktg5 vibrio chol
26	51	33.6	304	16	0930K5	0930k5 rhizobium m
27	51	33.6	457	5	09NTP5	09ntp5 strongyloce
28	50	32.9	365	16	P71599	P71599 mycobacteri
29	50	32.9	579	4	09PT83	09pt83 homo sapien
30	50	32.9	667	11	0924H2	0924h2 mus musculu
31	50	32.9	746	4	096RNS	096rns homo sapien
32	50	32.9	748	4	096CT0	096ct0 homo sapien
33	50	32.9	1454	4	060244	060244 homo sapien
34	50	32.9	1454	4	09UNB3	09unb3 homo sapien
35	50	32.9	3175	12	091DM2	091dm2 equine arte
36	49	32.2	230	16	09KM56	09km56 vibrio chol
37	49	32.2	458	5	015996	015996 hemiceleotrot
38	49	32.2	543	16	09KSF8	09ksf8 vibrio chol
39	49	32.2	651	10	022042	022042 arabidopsis
40	49	32.2	1130	5	020661	020661 caenorhabdi
41	48.5	31.9	240	5	020417	020417 caenorhabdi
42	48	31.6	441	2	069192	069192 listeria in
43	48	31.6	441	16	0928V0	0928v0 drosophila
44	48	31.6	595	5	09VFW6	09vfw6 drosophila
45	47.5	31.2	155	3	074353	074353 schizosacch

## ALIGNMENTS

RESULT 1

09C001 PRELIMINARY: PRT: 150 AA.

AC 09C001;

DT 01-JUN-2001 (TREMBLrel, 17, Created)

DT 01-JUN-2001 (TREMBLrel, 17, last sequence update)

DT 01-DEC-2001 (TREMBLrel, 19, last annotation update)

DE INTERLEUKIN-2 (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-20545237; PubMed-11093171;

RA Matesanz F., Delgado C., Fresno M., Alcina A.;

RT \*Allelic selection of human IL-2 gene.\*;

RL Eur. J. Immunol. 30:3516-3521(2000).

DR EMBL: AF228636; AAC53575.1; -.

DR HSSP: P01585; 31NK.

DR InterPro: IPR000779; Interleukin-2.

DR Pfam: PF00715; IL2; 1.

DR PRINTS: PR00265; INTERLEUKIN2.

DR ProDom: PD003649; Interleukin-2; 1.

DR SMART: SM00189; IL2; 1.

DR PROSITE: PS00424; INTERLEUKIN\_2; 1.

FT NON-TER 150

SQ SEQUENCE 150 AA; 17312 MW; BF25860FB836ACES CRC64;

Query Match 96.7%; Score 147; DB 4; Length 150;  
Best Local Similarity 100.0%; Pred. No. 1.6e-14;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APTSSSTKKTQQLQLEHLLDLQMLINGINN 31  
Db 21 APTSSSTKKTQQLQLEHLLDLQMLINGINN 50

RESULT 2

```

O9XS38
ID O9XS38 PRELIMINARY; PRT; 154 AA.
AC O9XS38;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE IL-2.
OS Papio hamadryas (Hamadryas baboon),
OS Aotus lemurinus (Northern gray-necked night monkey),
OS Aotus nancymae (Owl monkey),
OS Aotus nigripes (black-headed night monkey), and
OS Aotus vociferans (noisy night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557, 43147, 37293, 57175, 57176;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
RA Patirroyo M.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U88365; AAD41538.1; -
DR EMBL: U88364; AAD41534.1; -
DR EMBL: U88361; AAD41535.1; -
DR EMBL: U88363; AAD41536.1; -
DR EMBL: U88362; AAD41537.1; -
DR HSSP: P01585; 31NK.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam: PF00715; IL2; 1.
DR PRINTS: PRO0265; INTERLEUKIN2.
DR PRODOM: PD003649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
DR PROSITE: PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17675 MW; AB752ABADA96469 CRC64;

Query Match 95.4%; Score 145; DB 6; Length 154;
Best Local Similarity 96.7%; Pred. No. 3,3e-14;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLOLEHLLDLMILGINN 31
DB 21 APTSSSTKKTQLOLEHLLDLMILGINN 50

RESULT 3
O3169 PRELIMINARY; PRT; 156 AA.
ID O3169;
AC O3169;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE INTERLEUKIN 2.
GN IL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu D., Wu Y., Chen J., Yu L., Zhong M., Hu L., Qu H.;
RT "Expression of human IL-2 from gene transferred mouse melanoma cells
and its effect on the growth of mouse melanoma.";
RL Chung-Hua Min Kuo Wei Sheng Wu Chi Mien I Hsueh Tsa Chih
RL 13:78-82(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Xu L.;
RT Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U25676; AAA70092.1; -
DR HSSP: P01585; 31NK.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam: PF00715; IL2; 1.
DR PRINTS: PRO0265; INTERLEUKIN2.

```

```

DR PRODOM: PD003649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
DR PROSITE: PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 156 AA; 18002 MW; 8E0452D43B336389 CRC64;

Query Match 89.1%; Score 135.5; DB 4; Length 156;
Best Local Similarity 90.9%; Pred. No. 9,3e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

OY 2 APTSSSTKKTQLOLEHLLDLMILGINN 31
DB 21 APTSSSTKKTQLOLEHLLDLMILGINN 53

RESULT 4
O16334 PRELIMINARY; PRT; 139 AA.
ID O16334;
AC O16334;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE IL-2 PROTEIN (FRAGMENT).
GN IL-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-95239150; PubMed-7722480;
RA Elzenberg O., Faber-Elman A., Lotan M., Schwartz M.;
RT "Interleukin-2 transcripts in human and rodent brains: possible
expression by astrocytes.";
RL J. Neurochem. 64:1928-1936(1995).
DR EMBL: S77835; AAD14264.1; -
DR HSSP: P01585; 31NK.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam: PF00715; IL2; 1.
DR PRINTS: PRO0265; INTERLEUKIN2.
DR PRODOM: PD003649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
DR PROSITE: PS00424; INTERLEUKIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 139 AA; 15986 MW; 731FBA406D0C63C5 CRC64;

Query Match 88.2%; Score 134; DB 4; Length 139;
Best Local Similarity 93.3%; Pred. No. 1,4e-12;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLOLEHLLDLMILGINN 31
DB 17 APTSSSTKKTQLOLEHLLDLMILGINN 46

RESULT 5
O9X783 PRELIMINARY; PRT; 155 AA.
ID O9X783;
AC O9X783;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE INTERLEUKIN 2.
OS Halichoerus grypus (Gray seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Halichoerus.
OX NCBI_TaxID=9711;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-99221046; PubMed-10206205;
RA St-Laurent G., Bellevue C., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
(Delphinapterus leucas) and grey seal (Halichoerus grypus) Interleukin
2.";

```



```

RL Vet. Immunol. Immunopathol. 67:385-394(1999).
DR EMBL: AF072871; AAD40848.1; -.
DR HSSP: P01585; 31NK.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam: PF00715; IL2; 1.
DR PRINTS: PR00265; INTERLEUKIN2.
DR ProDom: PD003649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
DR PROSITE: PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 155 AA; 17860 MW; F18FA49AC6722A1A CRC64;

Query Match 71.4%; Score 108.5; DB 6; Length 155;
Best Local Similarity 74.2%; Pred. No. 1.2e-08;
Matches 23; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

OY 2 AP-TSSSTKKTQLEHLLDLQMLINGINN 31
   |||||||:|:| |||||:|:|:|:|:|
Db 21 APTSSSTKKTQEQMEQLLDLQLLNGVNN 51

RESULT 6
O9BG74 PRELIMINARY; PRT; 66 AA.
AC O9BG74;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERLEUKIN 2 (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RT "Expression of canine Interleukin-2 mRNA in concanavalin A-stimulated
   canine lymphocytes."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF333117; AAK01437.1; -.
DR HSSP: P01585; 1IRL.
DR InterPro: IPR000779; Interleukin-2.
DR PRINTS: PR00265; INTERLEUKIN2.
DR ProDom: PD003649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
DR NON_TER 1
FT NON_TER 66
SQ SEQUENCE 66 AA; 7389 MW; 22A893F79DA2AE47 CRC64;

Query Match 70.7%; Score 107.5; DB 6; Length 66;
Best Local Similarity 71.0%; Pred. No. 7e-09;
Matches 22; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

OY 2 AP-TSSSTKKTQLEHLLDLQMLINGINN 31
   |||||||:|:| |||||:|:|:|:|:|
Db 14 APTSSSTKKTQEQMEQLLDLQLLNGVNN 44

RESULT 7
O9TV12 PRELIMINARY; PRT; 79 AA.
AC O9TV12;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE INTERLEUKIN-2 (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;

```

```

RT "Cloning and sequencing of canine IL-2."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF091131; AAD46989.1; -.
DR HSSP: P01585; 1IRL.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam: PF00715; IL2; 1.
DR PRINTS: PR00265; INTERLEUKIN2.
DR ProDom: PD003649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
DR PROSITE: PS00424; INTERLEUKIN_2; 1.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9087 MW; 83079BF8FA659BD CRC64;

Query Match 70.4%; Score 107; DB 6; Length 79;
Best Local Similarity 71.4%; Pred. No. 1e-08;
Matches 20; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 4 TSSSTKKTQLEHLLDLQMLINGINN 31
   |||||||:|:| |||||:|:|:|:|:|
Db 7 TSSSTKKTQEQMEQLLDLQLLNGVNN 34

RESULT 8
O9MZR9 PRELIMINARY; PRT; 133 AA.
AC O9MZR9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERLEUKIN 2 VARIANT IL2DELTA2.
GN IL-2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN, LYMPH NODE;
RX MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
   European rabbit (Oryctolagus cuniculus).";
RL CytoKine 12:555-565(2000).
DR EMBL: AF169168; AAF86652.1; -.
DR HSSP: P01585; 31NK.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam: PF00715; IL2; 1.
DR ProDom: PD003649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
DR PROSITE: PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 133 AA; 14748 MW; 0D54758C190B5655 CRC64;

Query Match 69.7%; Score 106; DB 6; Length 133;
Best Local Similarity 72.4%; Pred. No. 2.4e-08;
Matches 21; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 APTSSSTKKTQLEHLLDLQMLINGINN 30
   |||||||:|:| |||||:|:|:|:|:|
Db 21 APTSSSTKKTQEQMEQLLDLQLVLLKGVN 49

RESULT 9
O923T2 PRELIMINARY; PRT; 155 AA.
AC O923T2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERLEUKIN 2.
OS Sigmodon hispidus (hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Sigmodontinae;

```

OC Sigmodon.  
 OX NCBI\_TaxID=42415;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Dannel M.R., Pleteva L.M., Langley R.J., Blanco J.C., Prince G.A.:  
 RT "Cloning, expression and purification of cotton rat IL-2."  
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF398349; AAK94012.1;  
 SO SEQUENCE 155 AA; 17627 MW; ACADDA65E993291 CRC64;

Query Match 69.7%; Score 106; DB 11; Length 155;  
 Best Local Similarity 73.3%; Pred. No. 2.8e-08;  
 Matches 22; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDQMLNGINN 31  
 Db 21 APTSSSTKKTQLEHLLDQMLNGINN 50

RESULT 10  
 ID 070329 PRELIMINARY; PRT; 138 AA.  
 AC 070329;  
 DT 01-AUG-1998 (TREMBlrel. 07, Created)  
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
 DE INTERLEUKIN-2 (FRAGMENT).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98234044; PubMed=9573100;  
 RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.:  
 RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and  
 RT analysis of cytokine mRNA expression in experimental visceral  
 RL leishmaniasis."  
 RL Infect. Immun. 66:2135-2142(1998).  
 DR EMBL: AF046212; AAC40097.1;  
 DR HSSP: P01585; 31NK.  
 DR InterPro: IPR000779; Interleukin-2.  
 DR Pfam: PF00715; IL2; 1.  
 DR PRINTS: PR00265; INTERLEUKIN2.  
 DR ProDom: PD003649; Interleukin-2; 1.  
 DR SMART: SM00189; IL2; 1.  
 DR PROSITE: PS00424; INTERLEUKIN\_2; 1.  
 FT NON\_TER 1  
 FT 138  
 SO SEQUENCE 138 AA; 15739 MW; 351032995B670779 CRC64;

Query Match 67.8%; Score 103; DB 11; Length 138;  
 Best Local Similarity 73.3%; Pred. No. 7.1e-08;  
 Matches 22; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDQMLNGINN 31  
 Db 14 APTSSSTKKTQLEHLLDQMLNGINN 43

RESULT 11  
 ID 090CF5 PRELIMINARY; PRT; 23 AA.  
 AC 090CF5;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE INTERLEUKIN 2 (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93289963; PubMed=8512072;  
 RA Mullner S., Karbe-Thonges B., Tripiet D.:  
 RT "Charge heterogeneity of insulin fusion proteins expressed in  
 RT Escherichia coli is not due to proteolytic degradation."  
 RL Anal. Biochem. 210:366-373(1993).  
 SO SEQUENCE 23 AA; 2637 MW; 40B64C6875CE021F CRC64;

Query Match 59.9%; Score 91; DB 4; Length 23;  
 Best Local Similarity 90.5%; Pred. No. 7.7e-07;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TSSSTKKTQLEHLLDQML 24  
 Db 3 TSSSTKKTQLEHLLDQML 23

RESULT 12  
 ID 09XT84 PRELIMINARY; PRT; 154 AA.  
 AC 09XT84;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE INTERLEUKIN 2.  
 OS Delphinapterus leucas (beluga whale).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;  
 OC Monodontidae; Delphinapterus.  
 OX NCBI\_TaxID=9749;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99221046; PubMed=10206205;  
 RA St-Laurent G., Belliveau C., Archambault D.:  
 RT "Molecular cloning and phylogenetic analysis of beluga whale  
 RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) Interleukin  
 RT 2."  
 RL Vet. Immunol. Immunopathol. 67:385-394(1999).  
 DR EMBL: AF072870; AAD40847.1;  
 DR HSSP: P01585; 31NK.  
 DR InterPro: IPR000779; Interleukin-2.  
 DR Pfam: PF00715; IL2; 1.  
 DR PRINTS: PR00265; INTERLEUKIN2.  
 DR ProDom: PD003649; Interleukin-2; 1.  
 DR SMART: SM00189; IL2; 1.  
 DR PROSITE: PS00424; INTERLEUKIN\_2; 1.  
 SO SEQUENCE 154 AA; 17652 MW; 4288D3D41D04F172 CRC64;

Query Match 54.6%; Score 83; DB 6; Length 154;  
 Best Local Similarity 56.7%; Pred. No. 8.7e-05;  
 Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDQMLNGINN 31  
 Db 21 APTSSSTKKTQLEHLLDQMLNGINN 50

RESULT 13  
 ID 088210 PRELIMINARY; PRT; 152 AA.  
 AC 088210;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
 DE INTERLEUKIN 2 PRECURSOR.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.

```

RC TISSUE-SPLEEN;
RA Takeyoshi M., Iwata H., Inoue T.;
RL "Guinea pig Interleukin 2(IL-2) precursor.";
RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB010093; BAA31346.1;
DR HSSP: P01585; 1IRL.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam: PF00715; IL2; 1.
DR PRINTS: PR00265; INTERLEUKIN2.
DR ProDom: PD003649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
KM Signal.
FT CHAIN 21 152 POTENTIAL.
FT SEQUENCE 152 AA: 17271 MW; CATAC08C1BDD1FA CRC64;

QY Query Match 53.9%; Score 82; DB 11; Length 152;
Best local Similarity 60.0%; Pred. No. 0.00012;
Matches 18; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

DB 21 APTSSSTGNTMKVKSLLDLQLLGKVN 50

RESULT 14
Q9GJR4 PRELIMINARY: PRT: 69 AA.
AC Q9GJR4;
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE INTERLEUKIN 2 PRECURSOR (FRAGMENT).
GN IL-2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-SHEEP 2, AND SHEEP 1;
RL Luehken G., Prinzberg E.-M., Hienfelder S., Erhardt G.;
RT "A single strand conformation polymorphism in the ovine interleukin 2
(RT (IL-2) gene.";
RL J. Anim. Sci. 0:0-0(2000).
DR EMBL: AF215687; AAG43986.1;
DR EMBL: AF215683; AAG35709.1;
DR HSSP: P01585; 1IRL.
DR InterPro: IPR000779; Interleukin-2.
DR PRINTS: PR00265; INTERLEUKIN2.
DR ProDom: PD003649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
KM Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 >69 INTERLEUKIN 2.
FT NON_TER 69
SQ SEQUENCE 69 AA: 7711 MW; B8768C23BB34D1AE CRC64;

QY Query Match 52.0%; Score 79; DB 6; Length 69;
Best local Similarity 53.3%; Pred. No. 0.00016;
Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

DB 21 APTSSSTGNTMKVKSLLDLQLLGKVN 50

RESULT 15
Q9GLB3 PRELIMINARY: PRT: 155 AA.
AC Q9GLB3;
DT 01-MAR-2001 (TRENBLREL. 16, Created)

```

```

DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE INTERLEUKIN 2.
GN IL-2.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA ying Q.H., Li X.R., Pan J.Y.;
RT "Cloning of the goat IL-2 gene and its expression in E.coli.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307018; AAG28783.1;
DR HSSP: P01585; 3INK.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam: PF00715; IL2; 1.
DR PRINTS: PR00265; INTERLEUKIN2.
DR ProDom: PD003649; Interleukin-2; 1.
DR SMART: SM00189; IL2; 1.
DR PROSITE: PS00424; INTERLEUKIN-2; 1.
SQ SEQUENCE 155 AA: 17605 MW; EEBB2DE18F5469AA CRC64;

QY Query Match 52.0%; Score 79; DB 6; Length 155;
Best local Similarity 53.3%; Pred. No. 0.00035;
Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

DB 21 APTSSSTGNTMKVKSLLDLQLLGKVN 50

```

Search completed: October 25, 2002, 15:49:24  
Job time : 28 secs

